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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:16:10 ; Search time 22 seconds

(without alignments)
840.095 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874
Sequence: 1 MGFLTLAKLNNELHGOES.....RSLQSVRSEVRIYDYTDV 358Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pap:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pap:*
- 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pap:*
- 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pap:*
- 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pap:*
- 6: /cgn2_6/ptodata/2/1aa/backfile1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1846	98.5	358	3	US-08-988-876-3
2	1846	98.5	358	4	US-09-919-172-22
3	768.5	41.0	338	3	US-08-988-876-8
4	768.5	41.0	338	3	US-09-303-524A-2
5	762.5	40.7	325	2	US-08-467-946A-29
6	762.5	40.7	325	2	US-08-467-947A-29
7	694.5	37.1	342	3	US-08-852-824-2
8	694.5	37.1	333	3	US-09-221-456-2
9	690.5	36.8	333	4	US-09-558-740-2
10	668.5	35.7	333	2	US-08-812-871-1
11	466	24.9	293	2	US-08-467-946A-6
12	466	24.9	293	3	US-08-467-947A-6
13	420.5	22.4	319	1	US-08-702-344-28
14	375.5	20.0	342	4	US-08-988-876-9
15	372	19.9	346	4	US-09-585-876-2
16	368.5	19.7	408	2	US-08-742-440A-6
17	360	18.2	326	1	US-08-118-270-39
18	360	19.2	326	5	PCT-US93-08528-39
19	360	19.2	339	4	US-09-170-496D-182
20	357	19.1	339	4	US-08-153-848-44
21	357	19.1	339	2	US-08-812-871-3
22	357	19.1	339	3	US-09-299-843A-44
23	357	19.1	339	4	US-09-088-337B-44
24	357	19.1	339	4	US-09-170-496D-32
25	357	19.1	339	5	PCT-US93-11153-44
26	357	19.1	339	5	PCT-US95-07180-2
27	350	18.7	395	1	US-08-097-938-5

28	350	18.7	395	1	US-08-476-000-5	Sequence 5, Appli
29	350	18.7	395	2	US-08-472-840-5	Sequence 5, Appli
30	350	18.7	395	1	US-08-476-976-5	Sequence 5, Appli
31	350	18.7	395	3	US-08-474-410-5	Sequence 5, Appli
32	350	18.7	398	1	US-08-097-938-6	Sequence 6, Appli
33	350	18.7	398	1	US-08-476-000-6	Sequence 6, Appli
34	350	18.7	398	1	US-08-472-840-6	Sequence 6, Appli
35	350	18.7	398	2	US-08-476-976-6	Sequence 6, Appli
36	350	18.7	398	3	US-08-474-410-6	Sequence 6, Appli
37	350	18.7	398	3	US-08-486-673B-6	Sequence 6, Appli
38	349	18.6	395	3	US-08-486-673B-2	Sequence 2, Appli
39	349	18.6	395	3	US-08-486-673B-5	Sequence 5, Appli
40	349	18.6	399	1	US-08-476-000-61	Sequence 61, Appli
41	349	18.6	399	1	US-08-472-840-61	Sequence 61, Appli
42	349	18.6	399	2	US-08-476-976-61	Sequence 61, Appli
43	349	18.6	399	3	US-08-474-410-61	Sequence 61, Appli
44	349	18.6	399	3	US-08-486-673B-61	Sequence 61, Appli
45	348	18.6	361	4	US-09-170-496D-206	Sequence 206, App

ALIGNMENTS

RESULT 1
US-08-988-876-3
Sequence 3, Application US/08988876

Patent No. 6063596

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Bandman, Olga

APPLICANT: Hillman, Jennifer L.

TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED

TITLE OF INVENTION: WITH IMMUNE RESPONSE

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/988,876

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.

REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0441 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO. 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: PROSTUT09

CLONE: 1650519

US-08-988-876-3

Query Match 98.5%; Score 1846; DB 3; Length 358;
 Best Local Similarity 98.6%; Pred. No. 3.8e-138;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFNLTAKLPNNELHGOESHNSGNRSDGPKNTTTHNEFDITVLPVLIIFVASITLN 60
 DB 1 MGFNLTAKLPNNELHGOESHNSGNRSDGPKNTTTHNEFDITVLPVLIIFVASITLN 60
 QY 61 GLAWIFPHIRNKTSFIPLYKNTIVADLIMLTFFPRIVHDAGFGPMYFKPILCRYSVL 120
 DB 61 GLAWIFPHIRNKTSFIPLYKNTIVADLIMLTFFPRIVHDAGFGPMYFKPILCRYSVL 120
 QY 121 FYANMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 DB 121 FYANMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRHYHKSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRHYHKSSROF 240
 QY 241 ISOSRKRKKNOSIRVVAVFTCPYHLCPHPTFSHDLRLDESADKILYYCKEITL 300
 DB 241 ISOSRKRKKNOSIRVVAVFTCPYHLCPHPTFSHDLRLDESADKILYYCKEITL 300
 QY 301 FLSACVCLDPIIYFPMCRSPSRRLFKKSNIRTRSSIRSLQSVRSEVRITYDYTDV 358
 DB 301 FLSACVCLDPIIYFPMCRSPSRRLFKKSNIRTRSSIRSLQSVRSEVRITYDYTDV 358

RESULT 2

US-09-919-172-22
 ; Sequence 22, Application US/09919172
 ; Patent No. 6673545
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, Mary
 ; TITLE OF INVENTION: PROSTATE CANCER MARKERS
 ; FILE REFERENCE: PA-0036 US
 ; CURRENT APPLICATION NUMBER: US/09/919,172
 ; CURRENT FILING DATE: 2001-07-30
 ; PRIOR APPLICATION NUMBER: 60/222,469
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 22
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc. feature
 ; OTHER INFORMATION: Incyte ID No. 6673545 1650519CD1
 ; US-09-919-172-22

Query Match 98.5%; Score 1846; DB 4; Length 358;
 Best Local Similarity 98.6%; Pred. No. 3.8e-138;
 Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MGFNLTAKLPNNELHGOESHNSGNRSDGPKNTTTHNEFDITVLPVLIIFVASITLN 60
 DB 1 MGFNLTAKLPNNELHGOESHNSGNRSDGPKNTTTHNEFDITVLPVLIIFVASITLN 60
 QY 61 GLAWIFPHIRNKTSFIPLYKNTIVADLIMLTFFPRIVHDAGFGPMYFKPILCRYSVL 120
 DB 61 GLAWIFPHIRNKTSFIPLYKNTIVADLIMLTFFPRIVHDAGFGPMYFKPILCRYSVL 120
 QY 121 FYANMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 DB 121 FYANMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVLSCVWVIMAVLSLPMIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRHYHKSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVILIGCYIAISRHYHKSSROF 240

QY 241 ISOSRKRKKNOSIRVVAVFTCPYHLCPHPTFSHDLRLDESADKILYYCKEITL 300
 DB 241 ISOSRKRKKNOSIRVVAVFTCPYHLCPHPTFSHDLRLDESADKILYYCKEITL 300
 QY 301 FLSACVCLDPIIYFPMCRSPSRRLFKKSNIRTRSSIRSLQSVRSEVRITYDYTDV 358
 DB 301 FLSACVCLDPIIYFPMCRSPSRRLFKKSNIRTRSSIRSLQSVRSEVRITYDYTDV 358

RESULT 3

US-08-988-876-8
 ; Sequence 8, Application US/08988876
 ; Patent No. 6063596
 ; GENERAL INFORMATION:
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Bandman, Olga
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Yue, Henry
 ; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
 ; TITLE OF INVENTION: WITH IMMUNE RESPONSE
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/988,876
 ; FILING DATE: Herewith
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Billings, Lucy J.
 ; REGISTRATION NUMBER: 36,749
 ; REFERENCE/DOCKET NUMBER: PF-0441 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 338 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: Genbank
 ; CLONE: 285995
 ; US-08-988-876-8

Query Match 41.0%; Score 768.5; DB 3; Length 338;
 Best Local Similarity 47.6%; Pred. No. 2.9e-53;
 Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

QY 44 VLPLVLIIFVASITLNLGLAWIFPHIRNKTSFIPLYKNTIVADLIMLTFFPRIVHDAG 103
 DB 24 IIPVLICMWFITAGILNGVSGMIFPVPSKSTIYLKNTIVADLIMLTFFPRIVHDAG 83
 QY 104 FGPWFYFKILCRYSVLFYANMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVL 163
 DB 84 LGMQNLNVPFCRISAVLFTYNNMYTSIVFLGLSIDRYLKVVKPFGDSRMYSITFTKVL 143
 QY 164 CWMVIAVLSLPMIILITNGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVIL 223
 DB 164 CWMVIAVLSLPMIILITNGOPTEDNIHDCSKLSPGVKMTAVTVVNSCLFVAVLVIL 223

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Db      144  IVMMLMLLAVERNILITNOSVREVTQIKCIELKSELGRMKHANSYIFVAIFWIVFLILI 203
Qy      224  GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFETCFPLPHLCRIPTFSHLD 282
Db      204  VFTYATIKKIFKSHKSSRNSTSVKKSRIPIVFPVCFVPHIARIPTYSQTEA 263
Qy      283  LIDESAQILYYCKEITFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db      264  HYSOSKEILRYMKEFTLLLSAANVCDDPIIYFPLQCPREILCKKHIPLKAQNDLDS 323
Qy      343  SVRSEVR 351
Db      324  RIKRGNTTL 332

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RESULT 4
US-09-303-524A-2
; Sequence 2, Application US/09303524A
; Patent No. 6238873
; GENERAL INFORMATION:
; APPLICANT:
; APPLICANT: CHAMBERS, JONATHAN K.
; APPLICANT: STEWART, BRIAN R.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JIM
; APPLICANT: ARNOLD, ANNE ROMANIC
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
; FILE REFERENCE: GP50007
; CURRENT APPLICATION NUMBER: US/09/303,524A
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,957
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-303-524A-2

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Query Match      41.0%; Score 768.5; DB 3; Length 338;
Best Local Similarity 47.6%; Pred. No. 2,9e-53;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

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Qy      44  VLPVYLIIFFVASILNGLAWIFPHIRKTSFIYLNKIIVADIMTLTTPPRIVHDAG 103
Db      24  IIPVYXCVFIAGILNGLVSGWIFPVPSKSFIIYLNKIIVADIMTLTTPPRIVHDAG 83
Qy      104  FGPWFYKFLCRYSVLFYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSTTFKVLVS 163
Db      84  LGMQNLNVFCVSAVLFFVNMVYSIVFGLISPDYKIVKPLMTSFIQSYSKLSLV 143
Qy      164  CWMVMAVLSLPIIITNGOPTEDINHOSKSLPLGVKMHNAVYVNSCLFVAVLVILI 223
Db      144  IVMMLMLLAVERNILITNOSVREVTQIKCIELKSELGRMKHANSYIFVAIFWIVFLILI 203
Qy      224  GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFETCFPLPHLCRIPTFSHLD 282
Db      204  VFTYATIKKIFKSHKSSRNSTSVKKSRIPIVFPVCFVPHIARIPTYSQTEA 263
Qy      283  LIDESAQILYYCKEITFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db      264  HYSOSKEILRYMKEFTLLLSAANVCDDPIIYFPLQCPREILCKKHIPLKAQNDLDS 323
Qy      343  SVRSEVR 351
Db      324  RIKRGNTTL 332

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RESULT 5

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US-08-467-948A-29
; Sequence 29, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-467-948A-29

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Query Match      40.7%; Score 762.5; DB 2; Length 325;
Best Local Similarity 48.2%; Pred. No. 8,4e-53;
Matches 146; Conservative 63; Mismatches 93; Indels 1; Gaps 1;

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Qy      44  VLPVYLIIFFVASILNGLAWIFPHIRKTSFIYLNKIIVADIMTLTTPPRIVHDAG 103
Db      23  IIPVYXCVFIAGILNGLVSGWIFPVPSKSFIIYLNKIIVADIMTLTTPPRIVHDAG 82
Qy      104  FGPWFYKFLCRYSVLFYANNYSIVFLGLISIDRYLKVKVPFGDSRMYSTTFKVLVS 163
Db      83  LGMQNLNVFCVSAVLFFVNMVYSIVFGLISPDYKIVKPLMTSFIQSYSKLSLV 142
Qy      164  CWMVMAVLSLPIIITNGOPTEDINHOSKSLPLGVKMHNAVYVNSCLFVAVLVILI 223
Db      143  IVMMLMLLAVERNILITNOSVREVTQIKCIELKSELGRMKHANSYIFVAIFWIVFLILI 202
Qy      224  GCYIAISRYIHKS-RQFISOSRRKKNOSIRVVAVFETCFPLPHLCRIPTFSHLD 282
Db      203  VFTYATIKKIFKSHKSSRNSTSVKKSRIPIVFPVCFVPHIARIPTYSQTEA 262
Qy      283  LIDESAQILYYCKEITFLSACNVCDDPIIYFPMCRSFRLLFKKSNIRTSSESIRSIQ 342
Db      263  HYSOSKEILRYMKEFTLLLSAANVCDDPIIYFPLQCPREILCKKHIPLKAQNDLDS 322

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QY 343 SVR 345
Db 323 RIK 325

RESULT 6

US-08-467-947A-29
; Sequence 29, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR1
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,947A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEPPER, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-467-947A-29

Query Match 40.7%; Score 762.5; DB 3; Length 325;
Best Local Similarity 48.2%; Pred. No. 8.4e-53;
Matches 146; Conservative 63; Mismatches 93; Indels 1; Gaps 1;

QY 44 VLPVYLIIIVASIIILNGIAWIFPHINKTSFIYLYKNIVVADLIMLTTPPRIVHDAG 103
Db 23 IIPVLYCWFAGIILNGVSGWIFYPVSSKSFIIYLNKIVADVMSLTPEPKILGDSG 82
QY 104 FGPWFKEFLICRYTSVLFFYANNYTSIVFLGLISIDRYLKVVPFGDSWYSGITFKVLV 163
Db 83 LGPWQANFVCKVSAVLFYVMYVIVFGLISFPRYKIVKPLMTSTIQSVSISKLSLV 142
QY 164 CVMVIAVLSIPNIIITNGQPTEDNIHDSCKLSPGVKMTAVTVYVNSCLFVAVLVI 223
Db 143 IVMMLLAVNIIITNQSVEVTVQIKCIELKSELGRKMKASNYIVAVIFWIVFILLI 202
QY 224 GCYIAISRYIHKS--RQFISQSRKRKINSRVVAVFPCFLPHLCRIPFTFSHLDR 282

Db 203 VFTYATIKKIFKSHLKSRSNSTSVKKSSRNIFSVIFVPCVFPYHARIPYTSQTEA 262
QY 283 LIDESAQKILYCKEITLFLSACNVCLDPIIYFECRSFRRLLFKSNIRRSISIRLQ 342
Db 263 HYSQSKKEILRYMKEFTLLSNANVCIDPIIYFELCOFPREILCKKHLIPKAQNDLIS 322
QY 343 SVR 345
Db 323 RIK 325

RESULT 7

US-08-852-824-2
; Sequence 2, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 342
; TYPE: PRT
; ORGANISM: genomic
; US-08-852-824-2

Query Match 37.1%; Score 694.5; DB 3; Length 342;
Best Local Similarity 42.2%; Pred. No. 2e-47;
Matches 139; Conservative 68; Mismatches 113; Indels 9; Gaps 5;

QY 25 NRSQPGKNTL--HNEEDTIVLPVLYLIFVASIILNGIAWIFPHINKTSFIYLYK 81
Db 6 NLTSAPG-NISLCRDYKITQVLPPLTYVLFVGLITNGIAMRIFQIRSKSNFIYFLK 64
QY 82 NIVVADLIMLTTPPRIVHDAGRGPMYFKFLICRYTSVLFFYANNYTSIVFLGLISIRYL 141
Db 65 NTVISDLMLTTPPKILSDKLGCTGPRTFVCOVTSIVIFFTWYISISFGLITIRYQ 124
QY 142 KVPKFGDSRMYSITFKVLSVCVWVIMAVLSIPNIIITNGQPTEDNIHDSCKLSPGV 201
Db 125 KTRPFPKSNPKNLGKILSVIWMFPLSLPMLITRQPDQVKKCSFLKSEFGL 184
QY 202 KMTAVTVYVNSCLFVAVLIIIGCYIAISRYIHKS--SRQFISQSRKRKINSRVVA 259
Db 185 VMHEIVNYICQVIMINFLIYVICYTLITKELYSYVTRGVGKVPKR-KVNVAVFIIA 243
QY 260 VFTCPPLPYHLCRIPTFSHLDRLLDESQKILYCKEITLFLSACNVCLDPIIYFECR 319
Db 244 VFICFVFPFHARIPYLSQTRVDCTAENTLFTYVESITLMTLSNACDPIIYFPLCK 303
QY 320 SFSRRLFKSNIRRSISIRLSQVRSE 348
Db 304 SFRNSLI--SWLKCPNAGATSLSDQNRKKE 330

RESULT 8

US-09-221-456-2
; Sequence 2, Application US/09221456
; Patent No. 6162899
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HAUSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERS, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEA81 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia

STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
FILING DATE: 28-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,975
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70318-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-456-2

Query Match 36.8%; Score 690.5; DB 3; Length 333;
Best Local Similarity 41.1%; Pred. No. 4.1e-47;
Matches 127; Conservative 66; Mismatches 97; Indels 19; Gaps 4;

QY 33 NTTLHNEF-----DT---IVLPVLYLIIFVASILLNGLAWIFPHINKTSFIYYL 80
DB 2 NTTWOGFNRSERCRDRIVQLVFPALYTVFPLGILLNTLALWVFWHIPSSSTFIYYL 61
QY 81 KNIVVADLIMLTLPFRIVHDAGFGPMYFKFILCRYSVLFPANNYTSIVFLGISIDRY 140
DB 62 KNTLVADLIMLTLPFKILSDSHLAPWOLRAVFCRFSVITREYMGIVLGLIAFRF 121
QY 141 LKVVKPGDSRMYSITFTKVLVSCVWYIMAVLSLNNILTNQOPTEDNIDHCSKLSPG 200
DB 122 LKIRPLNIFLKKRVFAKTVSIFIMFPLFISLNTLSKKEATPSSVKKASLKGFLG 181
QY 201 VKHTAVTYVNSCLFVAVLVLLIGCYIAISRYIHKSROFISQSRKKNQSR----V 256
DB 182 LKHWQMVNNICQFIETVFIIMLVFYVVIYAKKYDSYRK--SKSKDKNNKKKLEGKVFV 238
QY 257 VVAVFPCFLPYHLCRIPTFSHLRLDLSAOKILYVCKEITFLSACVNCLEPIIYF 316
DB 239 VVAVFVCFAPFHARVPYTHSQTNKTKDCLQNLQFLAKETTLFLAATNLCMDPLIYF 298
QY 317 MCRSFSRRL 325
DB 299 LCKKFTKTL 307

RESULT 9
US-09-558-740-2
Sequence 2, Application US/09558740
Patent No. 6358695
GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HAUSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERS, PHILIP

TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE HNEAA81 RECEPTOR
FILE REFERENCE: GH-70318-2
CURRENT APPLICATION NUMBER: US/09/558,740
PRIOR FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match 36.8%; Score 690.5; DB 4; Length 333;
Best Local Similarity 41.1%; Pred. No. 4.1e-47;
Matches 127; Conservative 66; Mismatches 97; Indels 19; Gaps 4;

QY 33 NTTLHNEF-----DT---IVLPVLYLIIFVASILLNGLAWIFPHINKTSFIYYL 80
DB 2 NTTWOGFNRSERCRDRIVQLVFPALYTVFPLGILLNTLALWVFWHIPSSSTFIYYL 61
QY 81 KNIVVADLIMLTLPFRIVHDAGFGPMYFKFILCRYSVLFPANNYTSIVFLGISIDRY 140
DB 62 KNTLVADLIMLTLPFKILSDSHLAPWOLRAVFCRFSVITREYMGIVLGLIAFRF 121
QY 141 LKVVKPGDSRMYSITFTKVLVSCVWYIMAVLSLNNILTNQOPTEDNIDHCSKLSPG 200
DB 122 LKIRPLNIFLKKRVFAKTVSIFIMFPLFISLNTLSKKEATPSSVKKASLKGFLG 181
QY 201 VKHTAVTYVNSCLFVAVLVLLIGCYIAISRYIHKSROFISQSRKKNQSR----V 256
DB 182 LKHWQMVNNICQFIETVFIIMLVFYVVIYAKKYDSYRK--SKSKDKNNKKKLEGKVFV 238
QY 257 VVAVFPCFLPYHLCRIPTFSHLRLDLSAOKILYVCKEITFLSACVNCLEPIIYF 316
DB 239 VVAVFVCFAPFHARVPYTHSQTNKTKDCLQNLQFLAKETTLFLAATNLCMDPLIYF 298
QY 317 MCRSFSRRL 325
DB 299 LCKKFTKTL 307

RESULT 10
US-08-812-871-1
Sequence 1, Application US/08812871
Patent No. 5953303
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr.
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:

APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: MMLR3DT01
CLONE: 568987
US-08-812-871-1

Query Match 35.7%; Score 668.5; DB 2; Length 333;
Best Local Similarity 40.1%; Pred. No. 2.2e-45;
Matches 124; Conservative 67; Mismatches 99; Indels 19; Gaps 4;

33 NTTLHNEF-----DT-----IVLPVLIIFVASIILNGLAWVFPHIRKTSFIYL 80
2 NTVMGFNRSEKCPDRIIVQLVFPALTYVFTGLNTLALMWVFIHPSSTFIYL 61
81 KNIVADLIMTLTPFRIYHADGFGPWYFKILCRYSVLFYANMYSIVFLGLISIDRY 140
62 KNTLVADLIMTLMLPFKILSDSHLAPWQRAFCRFSVIFETMVGIVLGLIAPDRF 121
141 LKVVKPGDSRMYSITFTKVLSCVWVYNAVLSLPMIILTNQPTEDNHDCKSLKSPG 200
122 LKIRPLRNIFLKKPVWGTVSIFIFWFFISLPMIILSNKEATPSSVKKCASLKGPIG 181
201 VKMHTAVTVNSCLFVAVLVILIGCYIAISRYIHKSRSQFISSSRKRNOSIR----V 256
182 LKHHQVNNICQFIETVTLILMLVFYVIAKAYDSYRK---SKCKDRKNNKGLGKVPV 238
257 VVAVFTFCGLPYHLCHIFPTESHDLRLDESQKILYCKEITLFLSACNVLDPDIYF 316
239 VVPEFVFCAPHPHFAVVPYTHSQTNKKIDCRLOQLFAKETTLFLAATNLCMDPLISIF 298
317 MCRSFSRRL 325
299 LCKKFTKRL 307
DB

RESULT 11
US-08-467-948A-6
Sequence 6, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR2
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467, 948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEPP, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-948A-6

Query Match 24.9%; Score 466; DB 2; Length 293;
Best Local Similarity 40.3%; Pred. No. 1.8e-29;
Matches 85; Conservative 47; Mismatches 67; Indels 12; Gaps 2;

33 NTTLHNEF-----DT-----IVLPVLIIFVASIILNGLAWVFPHIRKTSFIYL 80
2 NTVMGFNRSEKCPDRIIVQLVFPALTYVFTGLNTLALMWVFIHPSSTFIYL 61
81 KNIVADLIMTLTPFRIYHADGFGPWYFKILCRYSVLFYANMYSIVFLGLISIDRY 140
62 KNTLVADLIMTLMLPFKILSDSHLAPWQRAFCRFSVIFETMVGIVLGLIAPDRF 121
141 LKVVKPGDSRMYSITFTKVLSCVWVYNAVLSLPMIILTNQPTEDNHDCKSLKSPG 200
122 LKIRPLRNIFLKKPVWGTVSIFIFWFFISLPMIILSNKEATPSSVKKCASLKGPIG 181
201 VKMHTAVTVNSCLFVAVLVILIGCYIAISRY 231
182 LKHHQVNNICQFIETVTLILMLVFYVIAK 212
DB

RESULT 12
US-08-467-947A-6
Sequence 6, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSER: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA: US/08/467, 947A
APPLICATION NUMBER: US/08/467, 947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 293 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-947A-6

Query Match 24.9%; Score 466; DB 3; Length 293;
Best Local Similarity 40.3%; Pred. No. 1.8e-29;
Matches 85; Conservative 47; Mismatches 67; Indels 12; Gaps 2;

Qy 33 NTLTNEP-----DT-----YLPVLYLIIFVASILNGLAWIFPHIRNKTSFIRYL 80
Db 2 NTTWAGNRSRCKPDRIVQLVLPALYTVFLGILLTALWVPHISSSTFIYL 61
Qy 81 KNIVADILMTLPFRIVHDAGFGPMYFKFLCYTSVLPFANNYTSIVPLGISIRY 140
Db 62 KNTLVADILMTLPFRIVHDAGFGPMYFKFLCYTSVLPFANNYTSIVPLGISIRY 121
Qy 141 LKVVAFGDSRMVSTFTFKVLSVCVWVMAVLSLNNIITLNGOPTEDNIDHCKSLKPLG 200
Db 122 LKTIPLNITLKKRWGKWTISIFWFWPFLSLNNIITLNGOPTEDNIDHCKSLKPLG 181
Qy 201 VKMHTAVTVNSCLFVAVLVILIGCYIAISR 231
Db 182 LKMHQVNNICQFIFWTVFILMLVYVVIK 212

RESULT 13
US-08-702-344-28
Sequence 28, Application US/08702344
Patent No. 5723315
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John
APPLICANT: Lavalley, Edward
APPLICANT: Racie, Lisa
APPLICANT: Merberg, David
APPLICANT: Treacy, Maurice
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
TITLE OF INVENTION: ENCODING THEM
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344

FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-344-28

Query Match 22.4%; Score 420.5; DB 1; Length 319;
Best Local Similarity 29.6%; Pred. No. 7.4e-26;
Matches 83; Conservative 64; Mismatches 126; Indels 7; Gaps 3;

Qy 49 YLIIFVASILNGLAWIFPHIR-NKTSFIRYKNIVADILMTLPFRIVHDAGFGPM 107
Db 21 FVLVFLVGLIGSCFATWAFIQNTNRCVSIYLLNLTADPLTLALPVKIVDGLVAPW 80
Qy 108 YFKRILCRYTSVLPFANNYTSIVPLGISIRYKLVKVPFDSRMVSTFTFKVLSVCVW 167
Db 81 KLFKFCQVTAQLYINMYLSIFLAFVSIIDRCLQTHSKIRYIOBDFGKMTSTVWL 140
Qy 168 IMAVLSLNNIITLNGOPTEDNIDHCKSLKPLGVMHTAVTVNSCLFV--AVLVILIGC 225
Db 141 MVLIMPNNMIPKIDIKESNNGCMFKFGKNNMLTTFICATLANSATILISNC 200
Qy 226 YIAISRYIKSSROFISOSRRKQNSIRVAVFTCLPYHLCRIPFESHLDRLD 285
Db 201 LVIRQLVNNKQNNY---PVKKALINILVTTGYIICFVPHYHVRIPYLSQTEVITD 256
Qy 286 ESAQKILYCKEITLFLSACVNCIDPITYFMCSPSRRL 325
Db 257 CSTRIISLFAKATLLAVSNLCEDPILYHLSKAFRSKV 296

RESULT 14
US-08-988-876-9
Sequence 9, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36, 749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 342 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 49443
US-08-988-876-9

Query Match      20.0%; Score 375.5; DB 3; Length 342;
Best Local Similarity 27.2%; Pred. No. 2,8e-22;
Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY 22 NSGNRSDGPKKNTLHNEPDTIVLPVLYLIFVASILNGLAVWTFPHI--RNKTSFIF 78
DB 4 NSSRVD-----SEFRYTLFPVYSIIFVLGINGVYLVFARLPSPKLNELKI 54
QY 79 YLKNIVADLIMLTLPFPRIVDHAGRPWYEFKFLICRYTSVLFYANMTSIVFLGLISD 138
DB 55 FFWNLTVADLFLITLPLWIVVYSNQGWFPLPKFLNLAGCLFINTYCSVAFGLVITYN 114
QY 139 RLKLVKPKPGDSRMYSITFTKVLSCVWYVIMASL-----VLSLPIIILNGOPTEDNIHD 191
DB 115 RFOAVKYPFKTQATTRKGIASLVIWVAIVAAASYFLVMDSTNVV--SKAAGSNITR 172
QY 192 CSKLSPLGKWHMTAVTVNSCL--FVAVLVILIGCYAISRVIKSSRQFISQSR-- 246
DB 173 CREHYE---KSKPLIHIICIVLGFIVFLILFCNLVI---IHTLLRQPVKQGNAE 225
QY 247 -RRKINOSIRVVAVFTGFLPYHLCRIPFTFSHLDRLLDESAQKILYCKEITLPLSAC 305
DB 226 VRRRALMWCTVLAVFVLCFVPHHWQLPWTLAEIG-MWPSNHOAINDAHQVTLCLST 284
QY 306 NVCLEPIITFEMCRSFRRLFKKSNIRTSSESIRSLQSVRSSEVRITYDYTDV 358
DB 285 NCVLPVLYCFLTKRKRLSEKLNIMSSQKCSRYTDTGTENALPINHTPV 337

RESULT 15
US-09-585-876-2
Sequence 2, Application US/09585876
Patent No. 6586205
GENERAL INFORMATION:
APPLICANT: Glucksmann, Maria Alexandra
APPLICANT: Silos-Santiago, Immaculada
TITLE OF INVENTION: 43239, A No. 6586205el GPCR-like Molecule and
TITLE OF INVENTION: Uses Thereof
FILE REFERENCE: 5800-88
CURRENT APPLICATION NUMBER: US/09/585,876
CURRENT FILING DATE: 2000-06-01
EARLIER APPLICATION NUMBER: 60/182,061
EARLIER FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 346
TYPE: PRT
ORGANISM: Homo sapiens
US-09-585-876-2

Query Match      19.9%; Score 372; DB 4; Length 346;
Best Local Similarity 28.4%; Pred. No. 5.3e-22;
Matches 98; Conservative 68; Mismatches 153; Indels 26; Gaps 10;

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QY 19 ESHNSGRSDGPKKNTLHNEPDTIVLPVLYLIFVASILNGLAVWTFPHI--RNKTSFIF 77
DB 16 EMEPNIGTFSNNNSRNCITEN-FKREFFIYLLIFFGVGLNGLSIVFLQPYKKSSTVN 74
QY 78 YLKNIVADLIMLTLPFPRIVDHAGRPWYEFKFLICRYTSVLFYANMTSIVFLGLISD 137
DB 75 VFMLNLASDILLFISTLPFRADYYLRGSSWIFGDLACRIMSYSILYVMYSIYFLVLSV 134
QY 138 DRYLKVYKPGDSRMYSITFTKVLSCVWYVIMASL-----VLSLPIIILNGOPTEDNIHD 191
DB 135 VRFLAMVHPFRLHVTISRSMILGIIWILIMASSI--MLDSGSQNGSVISCLELNL 192
QY 198 PLGVKWHYA--VTVNSCLFVAVLVILIGCYAISRVIKSSRQFISQSRKRKRNQSI 255
DB 193 YKIKLOTMTAYIALVVGCLPFFTLST--CYLLIRVLKYE--VPSGLRVSHRKALT 247
QY 256 VVV--AVFTGFLPYHLCRIPFTFSHLDRLLDESAQKILYCKEITLPLSACVCLDPI 312
DB 248 TIIITLIIFFLCFLPYHTLRTVHLTWKVGICKRDLHKALV---ITLVLAANAACFNPL 303
QY 313 IYFMCRSFSRRLFKKSNIR-----TRSESIRSLQSVRSSEVRITYDYTDV 351
DB 304 LYFAGENFKDRL--KSLRKRGHPQAKTKCVFPVSWLRKRETRV 346

Search completed: June 1, 2004, 15:19:51
Job time : 24 sec

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: June 1, 2004, 15:17:20 ; Search time 48 Seconds

(without alignments)
2082.736 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874

Sequence: 1 MGFNLTLLAKLNNELHGOES.....RSLQSVRSRVRIVYDITDV 358

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1151071 seqs, 279249464 residues

Total number of hits satisfying chosen parameters: 1151071

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1874	100.0	358	10	US-09-741-783-1
3	1874	100.0	358	12	US-10-165-844-1
4	1874	100.0	358	14	US-10-225-567A-418
5	1874	100.0	358	15	US-10-295-027-1255
6	1874	100.0	358	15	US-10-295-027-1255
7	1874	100.0	358	15	US-10-188-832-135
8	1874	100.0	358	16	US-10-692-605-18
9	1867	99.6	358	9	US-09-919-172-22
10	1846	98.5	358	9	US-09-974-298-86
11	1846	98.5	358	14	US-10-121-101B-1
12	889	47.4	196	15	US-10-264-237-2659
13	768.5	41.0	338	9	US-09-919-497-77
14	768.5	41.0	338	10	US-09-745-842-13
15	768.5	41.0	338	12	US-10-433-146-1

16	768.5	41.0	338	14	US-10-121-101B-10	Sequence 10, Appl
17	768.5	41.0	338	14	US-10-225-567A-213	Sequence 213, App
18	768.5	41.0	338	15	US-10-352-684A-42	Sequence 42, Appl
19	762.5	40.7	325	14	US-10-024-494-29	Sequence 29, Appl
20	742.5	39.6	338	9	US-09-826-508-20	Sequence 20, Appl
21	742.5	39.6	338	12	US-10-433-146-2	Sequence 2, Appl1
22	703.5	37.5	333	14	US-10-189-576-2	Sequence 2, Appl1
23	700.5	37.4	343	10	US-09-745-842-2	Sequence 2, Appl1
24	694.5	37.1	342	9	US-09-835-922-2	Sequence 2, Appl1
25	694.5	37.1	342	9	US-09-827-937A-2	Sequence 2, Appl1
26	694.5	37.1	342	9	US-09-780-576-2	Sequence 2, Appl1
27	694.5	37.1	342	9	US-09-964-008-1	Sequence 1, Appl1
28	694.5	37.1	342	10	US-09-745-842-6	Sequence 6, Appl1
29	694.5	37.1	342	12	US-09-875-076-32	Sequence 32, Appl
30	694.5	37.1	342	12	US-09-876-252-34	Sequence 34, Appl
31	694.5	37.1	342	12	US-10-343-550A-26	Sequence 26, Appl
32	694.5	37.1	342	14	US-10-225-567A-643	Sequence 643, App
33	694.5	37.1	342	14	US-10-333-844-2	Sequence 2, Appl1
34	694.5	37.1	342	14	US-10-272-983-32	Sequence 32, Appl
35	694.5	37.1	342	14	US-10-393-807-32	Sequence 32, Appl
36	694.5	37.1	342	15	US-10-417-820A-34	Sequence 34, Appl
37	692.5	37.0	315	10	US-09-745-842-4	Sequence 4, Appl1
38	692.5	37.0	333	10	US-09-924-125-2	Sequence 2, Appl1
39	692.5	37.0	333	10	US-09-957-187-2	Sequence 2, Appl1
40	692.5	37.0	333	14	US-10-243-106-2	Sequence 2, Appl1
41	692.5	37.0	333	14	US-10-225-567A-514	Sequence 514, App
42	692.5	37.0	333	15	US-10-352-684A-34	Sequence 34, Appl
43	692.5	37.0	333	15	US-10-308-968-2	Sequence 2, Appl1
44	692.5	37.0	333	16	US-10-692-605-8	Sequence 8, Appl1
45	690.5	36.8	333	9	US-09-769-159-2	Sequence 2, Appl1

ALIGNMENTS

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RESULT 1
US-09-826-508-10
; Sequence 10, Application US/09826508
; Patent No. US20010025099A1
;
GENERAL INFORMATION:
; APPLICANT: Nabil Elshourbagy
; TITLE OF INVENTION: G Protein-Coupled Receptor Polypeptides
; TITLE OF INVENTION: and Polynucleotides
; FILE REFERENCE: GP-7074AUSB
; CURRENT APPLICATION NUMBER: US/09/826,508
; CURRENT FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 358
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-826-508-10
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Query Match	100.0%	Score 1874;	DB 9;	Length 358;
Best Local Similarity	100.0%	Pred. No. 6.3e-162;	Indels 0;	Gaps 0;
Matches 358;	Conservative	0;	Mismatches 0;	
QY	1	MGFNLTLLAKLNNELHGOESHNSGNSRSDGPKNTTLLHNEFDITVL	PVLYLII	FVASILLN 60
DB	1	MGFNLTLLAKLNNELHGOESHNSGNSRSDGPKNTTLLHNEFDITVL	PVLYLII	FVASILLN 60
QY	61	GLAIVIFPHIRKRSFTLYLKNIVADIMLTTPFRIVHDAGFQPMWPKFLICRYTSVL		120
DB	61	GLAIVIFPHIRKRSFTLYLKNIVADIMLTTPFRIVHDAGFQPMWPKFLICRYTSVL		120
QY	121	FYANNYSIVFGLSISIRYLKVPKPDSDRYSITFKVLSCVWVIMAVLSLNIIT		180
DB	121	FYANNYSIVFGLSISIRYLKVPKPDSDRYSITFKVLSCVWVIMAVLSLNIIT		180
QY	181	NGOPTEDNIHDSKLSKSPLGVMHTAVTVYNSCLFVAVLIIIGCYIAISRYHKSROP		240

Db 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVYVNSCLFAVAVLILGCIYAIISRYIHKSROP 240
/ APPLICANT: Glucksmann, Maria A.
/ APPLICANT: Hodge, Martin R.
/ APPLICANT: Hunter, John J.
/ APPLICANT: Rudolph-Owen, Laura
/ APPLICANT: Weich, Nadine S.
/ APPLICANT: Siles-Santago, Inmaculada
/ TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding
/ FILE REFERENCE: 35800/248302
/ CURRENT APPLICATION NUMBER: US/10/165,844
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: US 09/088,857
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: US 09/324,465
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: US 09/464,685
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: US 09/741,783
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/145,745
/ PRIOR FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: US 09/383,745
/ PRIOR FILING DATE: 1999-08-26
/ PRIOR APPLICATION NUMBER: US 09/234,923
/ PRIOR FILING DATE: 1999-01-21
/ PRIOR APPLICATION NUMBER: US 09/340,880
/ PRIOR FILING DATE: 1999-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-741-783-1

RESULT 2

US-09-741-783-1
/ Sequence 1, Application US/09741783
/ Publication No. US20030162172A1
/ GENERAL INFORMATION:
/ APPLICANT: Glucksmann, Maria A.
/ APPLICANT: Hodge, Martin R.
/ APPLICANT: Hunter, John J.
/ APPLICANT: Rudolph-Owen, Laura
/ APPLICANT: Weich, Nadine S.
/ TITLE OF INVENTION: 2871 RECEPTOR, A NOVEL G-PROTEIN COUPLED RECEPTOR
/ FILE REFERENCE: 35800/207283
/ CURRENT APPLICATION NUMBER: US/09/741,783
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: 09/464,685
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: 09/324,465
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: 09/088,857
/ PRIOR FILING DATE: 1998-06-02
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-741-783-1

Query Match 100.0%; Score 1874; DB 10; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNPLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYIIFVASITL 60
DB 1 MGNPLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYIIFVASITL 60
QY 61 GLAWIFEFHIRNKTSIFLYLKNIVVADLIMTLTPPRIVHDAGPGPWYFKFLICRYT 120
DB 61 GLAWIFEFHIRNKTSIFLYLKNIVVADLIMTLTPPRIVHDAGPGPWYFKFLICRYT 120
QY 121 FYANMYTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSL 180
DB 121 FYANMYTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSL 180
QY 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVYVNSCLFAVAVLILGCIYAIISRYIHKSROP 240
DB 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVYVNSCLFAVAVLILGCIYAIISRYIHKSROP 240
QY 241 ISQSRKRKHNSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDLSAOKILYCKEITL 300
DB 241 ISQSRKRKHNSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDLSAOKILYCKEITL 300
QY 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
DB 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358

RESULT 3

US-10-165-844-1
/ Sequence 1, Application US/10165844
/ Publication No. US20030017539A1
/ GENERAL INFORMATION:

APPLICANT: Glucksmann, Maria Alexandra
/ APPLICANT: Hodge, Martin R.
/ APPLICANT: Hunter, John J.
/ APPLICANT: Rudolph-Owen, Laura
/ APPLICANT: Weich, Nadine S.
/ APPLICANT: Siles-Santago, Inmaculada
/ TITLE OF INVENTION: Novel Nucleic Acid Sequences Encoding
/ FILE REFERENCE: 35800/248302
/ CURRENT APPLICATION NUMBER: US/10/165,844
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: US 09/088,857
/ PRIOR FILING DATE: 1998-06-02
/ PRIOR APPLICATION NUMBER: US 09/324,465
/ PRIOR FILING DATE: 1999-06-02
/ PRIOR APPLICATION NUMBER: US 09/464,685
/ PRIOR FILING DATE: 1999-12-16
/ PRIOR APPLICATION NUMBER: US 09/741,783
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: US 09/145,745
/ PRIOR FILING DATE: 1998-09-02
/ PRIOR APPLICATION NUMBER: US 09/383,745
/ PRIOR FILING DATE: 1999-08-26
/ PRIOR APPLICATION NUMBER: US 09/234,923
/ PRIOR FILING DATE: 1999-01-21
/ PRIOR APPLICATION NUMBER: US 09/340,880
/ PRIOR FILING DATE: 1999-06-28
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1
/ LENGTH: 358
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-165-844-1

Query Match 100.0%; Score 1874; DB 12; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNPLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYIIFVASITL 60
DB 1 MGNPLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYIIFVASITL 60
QY 61 GLAWIFEFHIRNKTSIFLYLKNIVVADLIMTLTPPRIVHDAGPGPWYFKFLICRYT 120
DB 61 GLAWIFEFHIRNKTSIFLYLKNIVVADLIMTLTPPRIVHDAGPGPWYFKFLICRYT 120
QY 121 FYANMYTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSL 180
DB 121 FYANMYTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSL 180
QY 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVYVNSCLFAVAVLILGCIYAIISRYIHKSROP 240
DB 181 NGQPTEDNIDHCSKLSPLGVKMTAVTVYVNSCLFAVAVLILGCIYAIISRYIHKSROP 240
QY 241 ISQSRKRKHNSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDLSAOKILYCKEITL 300
DB 241 ISQSRKRKHNSIRVVAVVFTCFPLPYHLCRIPFTSHDRLLDLSAOKILYCKEITL 300
QY 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358
DB 301 FLASACNVCLDPIITYFPMCRSFSRRLFKKSNIRTRSESIRSLQSVRRSEVRIYYDYTDV 358

RESULT 4

US-10-225-567A-418
/ Sequence 418, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: Lifespan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenna C.
/ APPLICANT: Roush, Christine L.

TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 418
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-418

Query Match 100.0%; Score 1874; DB 14; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIFVASIILN 60
Db 1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIFVASIILN 60

Qy 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMWFKFLLCRYSVL 120
Db 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMWFKFLLCRYSVL 120

Qy 121 FYANNYSIVPLGLISIDRYLKVKRPFSDSMYSTTFPKVLSVCWVMIAVLSLNNIL 180
Db 121 FYANNYSIVPLGLISIDRYLKVKRPFSDSMYSTTFPKVLSVCWVMIAVLSLNNIL 180

Qy 181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
Db 181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240

Qy 241 ISQSRKKRKNQSIKRVVAVFETCPLPYHLCRIPFTFSLDRLDDESAOKILYYCKEITL 300
Db 241 ISQSRKKRKNQSIKRVVAVFETCPLPYHLCRIPFTFSLDRLDDESAOKILYYCKEITL 300

Qy 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSSEVRYYDYTDV 358
Db 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSSEVRYYDYTDV 358

RESULT 5
US-10-295-027-364
Sequence 364, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glen, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 364
LENGTH: 358
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-364

Query Match 100.0%; Score 1874; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 6,3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MGFNLTAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEFDITVLPVLYLIFVASIILN 60

Qy 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMWFKFLLCRYSVL 120
Db 61 GLAWIFPHIRNKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMWFKFLLCRYSVL 120

Qy 121 FYANNYSIVPLGLISIDRYLKVKRPFSDSMYSTTFPKVLSVCWVMIAVLSLNNIL 180
Db 121 FYANNYSIVPLGLISIDRYLKVKRPFSDSMYSTTFPKVLSVCWVMIAVLSLNNIL 180

Qy 181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240
Db 181 NGOPTEDNIHDCSKLSPGLGKMTAVTYVNSCLFVAVLVILIGCYIASRYIHKSROF 240

Qy 241 ISQSRKKRKNQSIKRVVAVFETCPLPYHLCRIPFTFSLDRLDDESAOKILYYCKEITL 300
Db 241 ISQSRKKRKNQSIKRVVAVFETCPLPYHLCRIPFTFSLDRLDDESAOKILYYCKEITL 300

Qy 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSSEVRYYDYTDV 358
Db 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQSVRSSEVRYYDYTDV 358

RESULT 6
US-10-295-027-1255
Sequence 1255, Application US/10295027
Publication No. US20030232350A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glen, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezi, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
FILE REFERENCE: 018501-012500US
CURRENT APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394

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; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 135
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1255

Query Match      100.0%; Score 1874; DB 15; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYLIIFVASILIN 60
DB 1 MGNNLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYLIIFVASILIN 60
QY 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTFPRIVHDAGFGPMYFKFLCRYSVL 120
DB 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTFPRIVHDAGFGPMYFKFLCRYSVL 120
QY 121 FYANNMTSIVPLGLISIDRYLKYVKGPGDSRMYSITFTKVLSCVWIMAVLSLPIIILT 180
DB 121 FYANNMTSIVPLGLISIDRYLKYVKGPGDSRMYSITFTKVLSCVWIMAVLSLPIIILT 180
QY 181 NGOPTEDNIDHSCSKLSPGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROF 240
DB 181 NGOPTEDNIDHSCSKLSPGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROF 240
QY 241 ISQSSRRKRNQSIIRVVAVVFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
DB 241 ISQSSRRKRNQSIIRVVAVVFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358

RESULT 7
US-10-188-832-135
; Sequence 135, Application US/10188832
; Publication No. US20040076955A1
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Nataeha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer. Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08

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; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 135
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-135

Query Match      100.0%; Score 1874; DB 16; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.3e-162;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGNNLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYLIIFVASILIN 60
DB 1 MGNNLTLAKLPNNELHGOESHNSGNSDGPKNITLHNEPDTIVLPVLYLIIFVASILIN 60
QY 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTFPRIVHDAGFGPMYFKFLCRYSVL 120
DB 61 GLAWIFPHIRNKTSIFLYLKNIVVADLIMTLTFPRIVHDAGFGPMYFKFLCRYSVL 120
QY 121 FYANNMTSIVPLGLISIDRYLKYVKGPGDSRMYSITFTKVLSCVWIMAVLSLPIIILT 180
DB 121 FYANNMTSIVPLGLISIDRYLKYVKGPGDSRMYSITFTKVLSCVWIMAVLSLPIIILT 180
QY 181 NGOPTEDNIDHSCSKLSPGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROF 240
DB 181 NGOPTEDNIDHSCSKLSPGVKMTAVTVVNSCLFVAVVILIGCYIAISRYIHKSROF 240
QY 241 ISQSSRRKRNQSIIRVVAVVFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
DB 241 ISQSSRRKRNQSIIRVVAVVFTCFPLPYHLCRIPTFTSHLDRLDESAQKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358
DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQVRSREVRYYDYTDV 358

RESULT 8
US-10-692-605-18
; Sequence 18, Application US/10692605
; Publication No. US20040091928A1
; GENERAL INFORMATION:
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; APPLICANT: Merchant, Kalpana
; TITLE OF INVENTION: G PROTEIN-COUPLED RECEPTORS EXPRESSED IN BRAIN
; FILE REFERENCE: 28341/6276 NX1
; CURRENT APPLICATION NUMBER: US/10/692,605
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: US 09/698,419
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 09/481,794
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 09/454,399
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: US 09/429,517
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,555
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,676
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/429,695
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: US 09/428,114
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/428,020
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 09/427,859
; PRIOR FILING DATE: 1999-10-27

```

Remaining Prior Application data removed - See file Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 18
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-692-605-18

Query Match 99.6%; Score 1867; DB 16; Length 358;
Best Local Similarity 99.6%; Pred. No. 2.7e-161;
Matches 357; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Db 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120
Qy 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Db 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Qy 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Db 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Qy 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Db 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Qy 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Db 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Qy 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358
Db 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358

RESULT 9

US-09-919-172-22
; Sequence 22, Application US/09919172
; Patent No. US20020119463A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 22
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020119463A1 1650519CD1
US-09-919-172-22

Query Match 98.5%; Score 1846; DB 9; Length 358;
Best Local Similarity 98.6%; Pred. No. 2.2e-159;
Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Db 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120

Qy 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Db 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Qy 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Db 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Qy 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Db 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Qy 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358
Db 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358

RESULT 10

US-09-974-298-86
; Sequence 86, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huel-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 86
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 1650519CD1
US-09-974-298-86

Query Match 98.5%; Score 1846; DB 9; Length 358;
Best Local Similarity 98.6%; Pred. No. 2.2e-159;
Matches 353; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Db 1 MGFNLTLLKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVLYLIIFVASIILN 60
Qy 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120
Db 61 GLAWWIFPHIRNKTSFIYLNKIIVVADLIMLTJPPFRIVHDAGFGPMWFKFILLCRYSVL 120
Qy 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Db 121 FYANNYSIVLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
Qy 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Db 181 NGOPTEDNIDHCSKSLKSPGVMHTAVYVNSCLFVAVLVILIGCYIAISRVIHKSROF 240
Qy 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Db 241 ISOSRRKKNQSIIRVVAVVFTGCLPYHLCRIPFTSHLDRLDESAQKILYYCKEITL 300
Qy 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358
Db 301 FLSACNVCLDPIIYFPMCRSFRSLFKKSNIRTSSESIIRLSQSVRSRVRRIYYDTDV 358

RESULT 11

US-10-121-101B-1
; Sequence 1, Application US/10121101B

Query Match	98.5%	Score 1846;	DB 14;	Length 358;
Best Local Similarity	98.6%	Pred. No. 2.2e-159;		
Matches 353; Conservative	2;	Mismatches 3;	Indels 0;	Gaps 0

RESULT 12
US-10-264-237-2659

```

? Sequence 2659, Application US/10264237
? Publication No. US20040009491A1
?
? GENERAL INFORMATION:
?
? APPLICANT: Bire et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: PAl31P1
? CURRENT APPLICATION NUMBER: US/10/264,237
? CURRENT FILING DATE: 2002-10-04
? PRIOR APPLICATION NUMBER: PCT/US01/16450
? PRIOR FILING DATE: 2001-05-18
? PRIOR APPLICATION NUMBER: US 60/205,515
? PRIOR FILING DATE: 2000-05-19
? NUMBER OF SEQ ID NOS: 2876
? SOFTWARE: PatentIn Ver. 3.1
? SEQ ID NO 2659
?
? LENGTH: 196
? TYPE: PRT

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Query Match	47.4%	Score 889;	DB 15;	Length 196;
Best Local Similarity	98.8%	Pred. No. 9.4e-73;		
Matches 170; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

Qy	1	MGPNLTLAKLIPNNELHOGESHNSGNRSDGPKNTLTLANEFDITVLPAVLYLIIFVASILLN	60
Db	1	MGPNLTLAKLIPNNELHOGESHNSGNRSDGPKNTLTLANEFDITVLPAVLYLIIFVASILLN	60
Qy	61	GLAWIIFPHIRNKSFIFYLKNIVVADILMPLTTPPRIVHDAGGPMYFKETILCRYTVL	120
Db	61	GLAWIIFPHIRNKSFIFYLKNIVVADILMPLTTPPRIVHDAGGPMYFKETILCRYTVL	120
Qy	121	FYANNYSIVELGISIDRYLKVKPGSDSMYSITTFKULSVCCWVMIAVL	172
Db	121	FYANNYSIVELGISIDRYLKVKPGSDSMYSITTFKULSVCCWVMIAVL	172

RESULT 13
US-09-919-497-77
; Sequence 77, Application US/09919497
; Patent No. US20020106662A1

```

1  APPLICANT: Muller, George L.
2  TITLE OR INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
3  FILE REFERENCE: B0801/7225
4  CURRENT APPLICATION NUMBER: US/09/919,497
5  CURRENT FILING DATE: 2001-07-31
6  PRIOR APPLICATION NUMBER: US 60/221,735
7  PRIOR FILING DATE: 2000-07-31
8  NUMBER OF SEQ ID NOS: 100
9  SOFTWARE: PatentIn version 3.0
10 SEQ ID NO 77
11
12 LENGTH: 338
13
14 TYPE: PRT
15
16 ORGANISM: Homo sapiens
17
18 US-09-919-497-77

```

Query Match 41.0%; Score 768.5; DB 9; Length 338;

Best Local Similarity 47.6%; Pred. NO. 1.6e-61;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1

```

Qy 44 VLPLVLLILFVASILLNGLAWIIFFIIRKRTSFICYLKNIVADLIMTLUPFFIIVHAG 103
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 24 IIVLVCMVFIAGIILLNGVSGMIFPVBSKSFIIYLNKIVADPVMSLTFPFMILLDSG 83
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 104 FGRWYFEFILCRTSLVFLFANMTYSIVFLGLISIDRYLKVKKPFEDSMHSITETKULSV 163
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 84 LGRWQNLNFCGRASALFVYNNVYSIVFEGLISPRYYKIKVPLMTSTISOVSXKLLSV 143
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 164 CWWVIMAVLSLPNIILTNQOPTEDNIHDSKLSPLGVKMHATAVYVNSCLEFVAVILI 223
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 144 IVMMLMLLAVPNIILTNQSVREVMQIKETELKELGRKMHKASNYIVPAIFWIVPILLI 203
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 224 GCYIAISRTHKES-RQFISQSSRRKKNQHSIRVVANVPFCPLPYHLICRIPIFFSHDR 282
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 204 VFTATATKFIKSHLSSRNSTSVKKSSSRNIFSVLPFCVFPYHARIPKYSQTEA 263
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 283 LLDPSAQKILYYCKEITLPLSACNVCLDPIIYFPMCRSPSRRLPFKSNIRTRSESISLQ 342
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 264 HYSQCSKEILRYMKETLLLSAANVCLDPIIYFPCQPFREILCKKLAIPIKAQNDIDIS 333
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy 343 SVRRSEVRI 351
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 324 RIRGRNTTL 332
   :::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

RESULT 14
US-09-745-842-13

Query Match	41.0%	Score 768.5	DB 10	Length 338
Best Local Similarity	47.6%	Pred. NO. 1.6e-61		
Matches 147	Conservative 64	Mismatches 97	Indels 1	Gaps 1

[illegible]

Db 204 VFETITKKIPFSLHKKSSRNSTSVYKKSSRNFSIVFVFCVCPHAIIRIIPYTKSQTEA 263

QY 203 LLDESAOKILYYCKEITFLSACVNCCLDPIIYFPMCRSPFRRLLPKFSNIRTRSEISRSIQ 342

Db 264 HYSQCSKILRYMKEFTLLSLANVCCLDPIIYFLDQCPREILCKLKLHPLKAGQNLDIS 323

QY 343 SVRSESVRI 351

Db 324 RIKRGNTTIL 332

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RESULT 15-146-1
US-10-433-146-1
; Sequence 1, Application US/104331146
; Publication NO. US20040072259A1
GENERAL INFORMATION:
APPLICANT: Scadden, David T.
APPLICANT: Lee, Byeong-Chel
TITLE OF INVENTION: METHODS AND PRODUCTS FOR MANIPULATING
TITLE OF INVENTION: HEMATOPOIETIC STEM CELLS
FILE REFERENCE: MO0765.70039.US
CURRENT APPLICATION NUMBER: US/10/433,146
CURRENT FILING DATE: 2003-05-30
PRIOR APPLICATION NUMBER: PCT/US01/45076
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: U.S. 60/250,727
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 338
TYPE: PRT
ORGANISM: Homo sapiens
US-10-433-146-1

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Query Match%	41.0%	Score 768.5;	DB 12;	Length 338;
Best Local Similarity	47.6%	Pred. No. 1.6e-61;		
Matches 147;	Conservative 64;	Mismatches 97;	Indels 1;	Gaps 1

[illegible]

Search completed: June 1, 2004, 15:20:51
Job time : 49 BECS

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 1, 2004, 15:14:35 ; Search time 20 seconds

(without alignments)
1721.828 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874

Sequence: 1 MGFLVTLAKLPNNELHGOES.....RSLQSVRSSEVRIYDVTDV 358

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR1:.*
2: PIR2:.*
3: PIR3:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	375.5	20.0	342	2	S13638 platelet-activatin
2	360	19.2	341	2	S43252 platelet-activatin
3	356.5	19.0	341	2	S63666 platelet activatin
4	349	18.6	399	2	I48705 proteinase activat
5	348.5	18.6	365	2	S68679 G protein-coupled
6	346	18.5	397	2	S66518 proteinase-activat
7	345	18.4	342	2	B45680 G protein-coupled
8	340.5	18.2	342	2	A40191 platelet-activatin
9	328	17.5	362	2	S33733 G protein-coupled
10	327	17.4	363	2	I57940 somatostatin recep
11	326	17.4	373	2	JC4162 P2Y receptor - bov
12	325	17.3	373	2	UC4737 G protein-coupled
13	324.5	17.3	373	2	AT4756 ATP receptor P2u -
14	324.5	17.3	420	2	I51667 thrombin receptor
15	321.5	17.2	308	2	I50241 G protein-coupled
16	320.5	17.1	352	2	I45747 neuropeptide Y/pep
17	313.5	16.7	352	2	G00048 fusin (leSTRA) - c
18	312.5	16.7	370	2	JC5549 heptanellical P2Y5-
19	311.5	16.6	375	2	A54946 P-2U nucleotide re
20	311.5	16.6	400	2	I56553 mu opiate receptor
21	311	16.6	428	2	S30508 probable G protein
22	310.5	16.6	398	2	I56517 mu opioid receptor
23	309.5	16.5	353	2	S28787 neuropeptide Y/pep
24	309.5	16.5	398	2	I56504 mu opioid receptor
25	309.5	16.5	398	2	A57510 mu opioid receptor
26	309	16.5	428	2	A44021 somatostatin recep
27	308	16.4	344	2	T09508 intron 17 purinerp
28	307	16.4	360	2	A57160 chemokine (C-C) re
29	306.5	16.4	363	2	I57955 somatostatin recep

30	306.5	16.4	392	2	S65693 oploid receptor mu
31	306	16.3	364	2	JN0763 somatostatin recep
32	305.5	16.3	418	2	A46226 somatostatin recep
33	305	16.2	380	2	A55259 kappa oploid recep
34	303	16.2	391	2	A39297 somatostatin recep
35	301.5	16.1	380	2	I38435 angiotensin II rec
36	301	16.1	359	2	S15403 angiotensin II rec
37	300.5	16.0	364	2	J01488 bradykinin B2 rece
38	300	16.0	391	2	A41795 somatostatin recep
39	300	16.0	391	2	C41795 somatostatin recep
40	298	15.9	356	2	I49340 MIP-1 alpha recept
41	296	15.8	359	2	I39418 angiotensin II rec
42	295.5	15.8	380	2	S36143 kappa oploid recep
43	295	15.7	350	2	A42009 N-formyl peptide r
44	295	15.7	380	2	JC2338 kappa oploid recep
45	294.5	15.7	380	2	A48227 kappa oploid recep

ALIGNMENTS

RESULT 1

S13638 platelet-activating factor receptor - guinea pig

C,Species: Cavia porcellus (guinea pig)

C,Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999

C,Accession: S13638

R,Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To

Nature 349, 342-346, 1991

A,Title: Cloning by functional expression of platelet-activating factor receptor from gu

A,Reference number: S13638; MUID:91101726; PMID:1846231

A,Accession: S13638

A,Status: preliminary

A,Molecule type: mRNA

A,Residues: 1-342 <HON>

A,Cross-references: GB:X56736; NID:949442; PIDN:CAA40060.1; PID:949443

A>Note: The species of guinea pig is not identified, in GenBank entry CCPARREC, release

C,Superfamily: ATP receptor P2u

Query Match 20.0%; Score 375.5; DB 2; Length 342;

Best Local Similarity 27.2%; Pred. No. 6.4e-25;

Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY	22	NSGNRSDGKNTLNHEDFTIVPVLXLIFFVASILNGLAVIFPHI---RMTKSTIF 78
DB	4	NSSSRVD-----SEFRYTLFPYVSIIFVGLIANGVAVLPARLPYSKKLNEIKI 54
QY	79	YLKQIVVADLIMTLTPPRIYVHDAGFGPWYFKFLICRYTSVLPYANMTYSIVPLQLS1D 138
DB	55	FMNULTVADLLFLTLPLMITYYNGQNWFLPKFLCNLAGCLFINTYCSVAFGLVITVN 114
QY	139	RYLVKVPFGDSRMYSITFTKVLSCVAVNA-----VLSLPIIITNCOPTEDN1HD 191
DB	115	RFQAVKYPKTAQQTTRKGIALLSLVIAVAASYFLVMDSTNVV---SNKAGSGPTR 172
QY	192	CSKLKSPFGVKNHATVYVNSCL---FAVAVIILGICIAISRYHKSRQFIQSSSR-- 246
DB	173	CFEYVE---GSKRPVLIHICIVLGFVYVLLILFCVLV---IHTLLRQPVKQORNAE 225
QY	247	-KRKNOSIRVVAVVFCTFLPYHLICRIPFTFSHLDRLDSSAOKILYYCKEITFLSAC 305
DB	226	VRRALMVCIVLAVFVFCFPHMVGQPLVLAELG--MPPSSNQAINDAQVTLCLIST 284
QY	306	NVCLDPIIYFMCSPFSRRLFKKSNITRSEISLSQSVRSSEVRIYDYDVTDV 358
DB	285	NCVLDPIVYCPFTKKFRKHLSEKLNIRSSQKSGRVTTDTGTMAIPINHPTV 337

RESULT 2

S43252 platelet-activating factor receptor - rat

C,Species: Rattus norvegicus (Norway rat)

C,Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 24-Nov-1999

C/Accession: S43252
 R/Bio: H.; Honda, Z.; Nakamura, M.; Shimizu, T.
 Eur. J. Biochem. 221, 211-218, 1994
 A/Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-
 A/Reference number: S43252; MUID:94222063; PMID:8168510
 A/Accession: S43252
 A/Molecule type: mRNA
 A/Residues: 1-341 <BIT>
 A/Cross-references: GB:U04740; NID:g470384; PIDN:AAA18422.1; PID:g470385
 C/Superfamily: ATP receptor P2u

Query Match 19.2%; Score 360; DB 2; Length 341;
 Best Local Similarity 28.7%; Pred. No. 1.4e-23;
 Matches 93; Conservative 63; Mismatches 134; Indels 34; Gaps 10;

QY 38 NEPDITLVPLVLLIFVASILNGLAVIF--FHINKTSFFLYLNIVADLIMTLTP 94
 DB 11 SEERYTLFPVIVSVIFLGVANGVYLVFATLYPSKKNLEIKIFMVNLTVALDLFLMTL 70
 QY 95 PFRIVDAGFGPMVFEKFLCRYSVLFFYANNYSIVFLGLISIDRYLKVKKP---GDS 150
 DB 71 PLMIVVYNSMGDMIVHKFLCNLAGCLFFINTYCSVAFLVITNRYQAVAPYIKTAQAT 130
 QY 151 RMTSITFTKVLSCVWVYVAVLSLNNITL--TNGOPTED--NIHDSKLSPLGVKMT 205
 DB 131 RKGKIT---LSLVIMISIMATASYFLATDSTINVPKDGSGNITRCFHYEFPYVPLV 186
 QY 206 AVTVNSCLFVAVLVILIGCYIAISRYHKSSNQFISQSSR---KKNHQSIRVVAVYF 262
 DB 187 VHLFITSCLFL-VFELIFYCNMVI---HTLTLRPVQRQKREKRRALMMCTVLAIVF 242
 QY 263 TCFPLPHLCRIPTFPHDLRLDDESAOKILYYCKEITLPLSACNVCLDPIYFMCRSFS 322
 DB 243 ICFVPHVAVQLPWTLAEIG--YQTNPHQAINDAHQITLLCLSTNCLDPIYICFLTKKR 300
 QY 323 RRLFKSNIRTRSESIRLSQVSR 346
 DB 301 KHL-----SEKFSWRSSRK 315

RESULT 3
 S63666
 platelet activating factor receptor - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S63666
 R/Bio: H.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.
 Biochem. J. 314, 671-678, 1996
 A/Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localiz
 A/Reference number: S63666; MUID:96239129; PMID:8670084
 A/Accession: S63666
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-341 <ISH>
 A/Cross-references: EMBL:D50872; NID:g1256924; PIDN:BA09468.1; PID:g1256925
 C/Superfamily: ATP receptor P2u

Query Match 19.0%; Score 356.5; DB 2; Length 341;
 Best Local Similarity 27.4%; Pred. No. 2.8e-23;
 Matches 93; Conservative 67; Mismatches 140; Indels 39; Gaps 10;

QY 21 HNSGRSDGPGKNTLHNEFDITVPLVYLLIFVASILNGLAVIFHT--RNKTSFI 77
 DB 3 HNGSRVD-----SEFRYTLFPVIVSVIFLGVANGVYLVFANLPSKKLEIK 53
 QY 78 FYLNIVVADLIMTLTPFRIVDAGFGPMVFEKFLCRYSVLFFYANNYSIVFLGLISI 137
 DB 54 IFMVNLTMADLFLITLPLMIVVYNNEDMLNPLCNVAGCLFFINTYCSVAFLGVITY 113
 QY 138 DRYLKVYKPGDSRMTSITFTKVLSCVWVYVAVLSLNNITL--TNGOPTED--NIH 190
 DB 114 NRYQAVAPYIKTAQATYTRKRGISLSLIMV--SIVATASYFLATDSTINVPKDGSGNIT 171

QY 191 DSKLSPLGVKMTAVTVNSCLFVAVLVILIGCYIAISRYHKSSROFISQSSR---K 247
 DB 172 RCFEHYEFPYVILVAVHFIACFEL-VFELIFYCNLVI---HTLTLQPRQQRKAGV 227
 QY 248 RQNGSIRVVAVFTCLPPLHLCRIPTFPHDLRLDDESAOKILYYCKEITLPLSACNV 307
 DB 228 RRLMMCTVLAIVFIFLCVPHVAVQLPWTLAEIG--YQTNPHQAINDAHQITLLCLSTNC 285
 QY 308 CLDPIYFMCRSFSRRLFKSNIRTRSESIRLSQVSR 346
 DB 286 VLDPIYCFELTKKFKHL-----SEKFSWRSSRK 315

RESULT 4
 148705
 proteinase activated receptor 2 - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
 C/Accession: 148705
 R/Bio: S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
 U. Biol. Chem. 270, 5950-5955, 1995
 A/Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
 A/Reference number: 148705; MUID:95197620; PMID:7890726
 A/Accession: 148705
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Residues: 1-399 <RES>
 A/Cross-references: EMBL:Z48043; NID:g663020; PIDN:CAA88097.1; PID:g663021
 C/Superfamily: ATP receptor P2u

Query Match 18.6%; Score 349; DB 2; Length 399;
 Best Local Similarity 27.0%; Pred. No. 1.5e-22;
 Matches 88; Conservative 72; Mismatches 136; Indels 30; Gaps 10;

QY 36 LHNEPDITLVPLVLLIFVASILNGLAVIF--FHINKTSFFLYLNIVADLIMTLTP 94
 DB 71 LTGKLTIVFLPVVYIIYFVIGLPSNGMALWIFLRTKKHAPVYVAVNMLADLLSVIWF 130
 QY 95 PFRIVDAGFGPMVFEKFLCRYSVLFFYANNYSIVFLGLISIDRYLKVKKPFGDSRMS 154
 DB 131 PLKISYHLHNNWYGBALCKVLIGFFYGMYSILFMCTLSVQRYVAVINPMGHPRK-K 189
 QY 155 ITFTKVLSCVWVYVAVLSLNNITL--TNGOPTED--NIHDSKLSPLGVKMTAVTV 210
 DB 190 ANIAGVSLAMWILFIVTIPLVYMQTIYIPALNITTCIDVLPREVVG-----DNF 242
 QY 211 NSCLFVAVLVILIGCYIAISRYI--HKSSROFISQSSRKKHQSIRVVV--AVFTCF 265
 DB 243 NYFLSLAIGVFLPPALITASAVYIMIKTLRSSAMDEHSEKRRQRAIRLLIITVLAIFYCF 302
 QY 266 LPYHLCRIPFTFPHDLRLDDESAOKILYYCKEITLPLSACNVCLDPIYFMCRSFSRL 325
 DB 303 APSTLLVAVYF-----LITQROSHVAVYVAVLCLSTNCLDPIYVYFVSKDF---- 353
 QY 326 FKSNIRTRSESIRLSQVSRSEVRI 351
 DB 354 --RDHAR-NALLCRSVTVNMQISL 376

RESULT 5
 S68679
 G protein-coupled receptor - human
 C/Species: Homo sapiens (man)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
 C/Accession: S68679
 R/Bio: N.J.; Klomp, J.; van de Heuvel, M.; Olijve, W.
 FEBS Lett. 384, 260-264, 1996
 A/Title: Molecular cloning and characterization of a novel orphan receptor (P2P) expe
 A/Reference number: S68679; MUID:96197801; PMID:8617367
 A/Accession: S68679
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-365 <STA>

321 PSR---RLEKSNIRTRRESIRS 340
 Db 315 YKKKMMRLKQVSVSISAVKS 337
 RESULT 8
 A40191
 platelet-activating factor receptor - human
 C.Species: Homo sapiens (man)
 C.Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
 C.Accession: A40191; JH0479; A41079; JCI359; A42831; I51923
 R.Kunz, D.; Gerard, N.P.; Gerard, C.
 J. Biol. Chem. 267, 9101-9106, 1992
 A.Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell sur-
 A.Reference number: A40191; MUID:92250505; PMID:1374385
 A.Accession: A40191
 A.Molecule type: mRNA
 A.Residues: 1-342 <KUN>
 A.Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
 R.Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.
 Biochem. Biophys. Res. Commun. 180, 105-111, 1991
 A.Title: Characterization of a human cDNA that encodes a functional receptor for platelet-
 A.Reference number: JH0479; MUID:92028922; PMID:1656963
 A.Accession: JH0479
 A.Molecule type: mRNA
 A.Residues: 1-342 <YER>
 A.Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
 A.Experimental source: granulocyte, cell line HL-60 all
 R.Nakamura, M.; Honda, Z.; Izumi, T.; Sakonaka, C.; Mutoh, H.; Minami, M.; Blto, H.; Sey-
 J. Biol. Chem. 266, 20400-20405, 1991
 A.Title: Molecular cloning and expression of platelet-activating factor receptor from hu-
 A.Reference number: A41079; MUID:92041873; PMID:1657923
 A.Accession: A41079
 A.Status: not compared with conceptual translation
 A.Molecule type: mRNA
 A.Residues: 1-342 <NKA>
 A.Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BA01050.1; PID:g219976
 R.Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
 Biochem. Biophys. Res. Commun. 189, 617-624, 1992
 A.Title: Molecular cloning and characterization of the platelet-activating factor recep-
 A.Reference number: JCI359; MUID:93112021; PMID:1281995
 A.Accession: JCI359
 A.Molecule type: mRNA
 A.Residues: 1-315, 'N', 317-342 <SUG>
 A.Experimental source: heart
 A.Note: the authors translated the codon AAT for residue 316 as Lys
 R.Seyfried, C.B.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
 Genomics 13, 832-834, 1992
 A.Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns
 A.Reference number: A42831; MUID:92347866; PMID:1322356
 A.Accession: A42831
 A.Molecule type: DNA
 A.Residues: 1-226, 'TG', 229-342 <SEY>
 A.Cross-references: GB:W81177; NID:g190697; PIDN:AAA60214.1; PID:g190698
 A.Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBI:P.109814)
 R.Chase, P.B.; Halonara, M.; Regan, J.W.
 Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
 A.Title: Cloning of a human platelet-activating factor receptor gene: evidence for an in-
 A.Reference number: I51923; MUID:93192035; PMID:8383507
 A.Accession: I51923
 A.Status: preliminary; translated from GB/EMBL/DBJ
 A.Molecule type: DNA
 A.Cross-references: GB:SS6396; NID:g298580; PIDN:AAB25755.1; PID:g298581
 C.Genetics:
 A.Gene: GDB:PTAFR
 A.Cross-references: GDB:128806; OMIM:173393
 A.Map position: 1p35-1p34.3
 A.Superfamily: ATP receptor P2u
 F.17/38/Domain: transmembrane #status predicted <TRI>
 F.154-75/Domain: transmembrane #status predicted <TRI>

F_92-113/Domain:	transmembrane	#status predicted <III>
F_134-155/Domain:	transmembrane	#status predicted <IV>
F_144-203/Domain:	transmembrane	#status predicted <TRV>
F_243-253/Domain:	transmembrane	#status predicted <IV>
F_277-297/Domain:	transmembrane	#status predicted <VII>

Query Match	18.2%;	Score 340.5;	DB 2;	Length 342;
Best Local Similarity	26.7%;	Pred. No. 6.8e-22;		
Matches	89;	Conservative	70;	Mismatches 139;
			Indels	35;
			Gaps	10;

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Oy 30 PGKNTLHNEPDTLVPLVYLIIIFASILLNGLAWIF---FHTIRKTSIFPKYKIVA 86
Dd 3 PHSSHMDEBFKTYLEPIYVSIILFVLGVIANGVYLMWPARLYPOCKNEIKIFMVMYTA 62
Oy 87 DLIMLTFFPRPIVHDAGRGPMYFKKILCKRYTSVLFYANMTSIVFGLISIDRYLKVVKP 146
Dd 63 DMLFLLTLELWLVYVQONGNMVLPRKLCNVAGCEFFINTYCSVAFGLVITYYNRQAVTRP 122
Oy 147 F-----GDSRMYSITFTKVLVSCVWMYIMVLSLPIIL--TNGQPT---EDNIDHC-----S 193
Dd 123 IKTAQNTKRRGIS-----LSLVIWALVIGASVYLLIDSTNTVPRDASGSGNVIRCFEHYE 178
Oy 194 KAKSPRLGVKMHPTAVYVNSCLFVAVLVLLIGCYTIALISRYIHKSROPTISQSSRRKKNOS 253
Dd 179 KGSVPYLI-IHFIYF---SFLVFLIILPCNVLVIRTLMLPVOOQRNAEYKRRLLMW 233
Oy 254 IRVVVAVFETCELPHLCRIPTFESHRLYLDSEAOKLUYCKEITLFLSACVNCDPPII 313
Dd 234 VCVLVAIVFLICVRHHVQLEPMTLAEIG-PQDSKPFQAIINDAHQVTLICLSTNCVLDPIV 292
Oy 314 YFPMCRSFSRRLPKKSNIRTSSESTRLSQSVRR 346
Dd 293 YCFLTKKPKFKH-----TEKYSYRRSSSRK 316

```

RESULT 9
S33733
G protein-coupled receptor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 24-Sep-1999
C:Accession: S33733
R:Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burnstock
FEBS Lett. 324, 219-225, 1993
A:Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A:Reference number: S33733; PMID:93285340; PMID:8508924
A:Accession: S33733
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-362 <WEB>
A:Cross-references: EMBL:X73268; NID:g395084; PIDD:CAA51716.1; PID:g395085
A:Superfamily: ATP receptor P2u
A:Keywords: G protein-coupled receptor; transmembrane protein

	Query Match	17.5%	Score 328;	DB 2;	Length 362;	
	Best Local Similarity	27.3%*	Pred. No. 8,6-21;			
	Matches	91;	Conservative	62;	Mismatches 130;	Indels 50; Gaps 12
Qy	40	EDTIVLPVLIITFVASILNLGLAVWIF-PHINKTSFIYLKNIYVADIIIMLTPEPRI	98			
Db	38	FQFYLPFTYIIVFITGFLGNSVAIWVFHFMRPWSGISYMNLLAFLPYLTLPAII	97			
Qy	99	VHDAGSGPYEKEILICRTSVLFAYNWTSTVPLGLSIDRYKYVKPFQDSMYSITEPT	158			
Db	98	FYYFNKTMBIFEDVNCCKLRPIFHNNLGSLILFTLCISVRHYGVVHPLKSLRLKKKA	157			
Qy	159	KVLSTCVWVIANVLSPNIIILTNQOPTEDN----IHDCSKLKSLPGVKMTAVTYVNS--	212			
Db	158	VVVSSLVMAIVAAVIAIP-ILFYGSGVRBNKTIICYDT-----TADEYLSRYF	204			
Qy	213	---C---LPAVALVILIGCY-LAIRYIHKSROPISSSRKRKNQSIIRVAVAFET	263			
	205	VYSMCTVFMFCIEPIRVIILGGYGLIALVALIKD---LDNSPLRRKSYIVVILIIVFAV	260			

Qy 264 CFLPYHL-----CRIPFESHLDRLDDESAOKILYYCKEITLPLASACNVCLDPIIYF 316
 Db 261 SYLPHVWKTNLRLARLDFOFQPMCAFMDC-----VATYQVTRGLASLNSGVDPILYFL 315
 Qy 317 MCRSFSRRLFKKSNIRTSSESIRLSQSVR-RSE 348
 Db 316 AGDTRRRRLSR-----ATRKSSRSRSEPNVQSKSE 344

RESULT 10

157940

Somatostatin receptor 5 - rat

N:Alternate names: somatotropin release-inhibiting factor subtype 28 receptor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 02-Aug-1996 #sequence revision 02-Aug-1996 #text_change 24-Nov-1999

C:Accession: 157940; 157949; S39244

R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 42, 939-946, 1992

A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pred

A:Reference number: 157940; MUID:93125499; PMID:1362243

A:Accession: 157940

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-363 <OCA1>

A:Cross-references: GB:I04535; NID:G409238; PIDN:AAA17029.1; PID:G409239

R:O'Carroll, A.M.; Lolait, S.J.; Konig, M.; Mahan, L.C.

Mol. Pharmacol. 44, 1278, 1993

A:Title: Molecular cloning and expression of a pituitary somatostatin receptor with pred

A:Reference number: 157949; MUID:94088493; PMID:8264565

A:Accession: 157949

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 341-363 <OCA2>

A:Cross-references: GB:S57370; NID:G455947; PIDN:AAB29371.1; PID:G455948

A:Experimental source: pituitary

R:Penhale, R.; Greenwood, M.; Patel, Y.C.

submitted to the EMBL Data Library, August 1993

A:Description: Correction of the nucleotide and amino acid sequence of the rat somatost

A:Reference number: 839244

A:Accession: S39244

A:Molecule type: mRNA

A:Residues: 309-363 <PEN>

A:Cross-references: EMBL:X74828; NID:G433911; PIDN:CAA52825.1; PID:G433912

C:Genetics:

A:Gene: SSTR5

C:Superfamily: vertebrate rhodopsin

Query Match 17.4%; Score 327; DB 2; Length 363;

Best Local Similarity 29.3%; Pred. No. 1.1e-20;

Matches 99; Conservative 62; Mismatches 139; Indels 38; Gaps 14;

Qy 5 LTLAKLPNNELHGOESHNSGNRSDGPKNTLLHNEFD-----TIVLPVLYLIIVASILL 59
 Db 4 LSLASTP-----SNNAASAASG-NHNWSLVGSASPMGARAVLVLPVLYLIVCTVGS 54
 Qy 60 NGLAWIIF-HIRNKTSTIFLYKNTVAVDLIMTLTFPRRIYHDAFGWYFELICRTS 118
 Db 55 NTLVLYVLRHAKMTVTNNVTLNLAADVLFMLDPLATONAAVSVWPGSFLCRLVM 114
 Qy 119 VLFYANMTSIVFLGLISIDRLKVKPFGDSRMYSITFTKVLSCVWVIMAVSLPNI 178
 Db 115 TLIDGNTSTIFCLMVMNVDRILAVVHPLRSARWRPRVAVASAAVAVFSLMSLP 174
 Qy 179 LTNQPTEDNIDGS-KLKSPLGVKMTA-VTVNSCLFVAVLVILICQYIAISRYIHS 236
 Db 175 PAD--VGEWGTCNLISWPEPVG-LWGAFAITYTSLVLFPGFLVICCYLLIVKV-KA 229
 Qy 237 SRQFISQSRK--KHNSIRVVVAVPTFCPLP--HICRIPTFSLHRLDDESAOK 290
 Db 230 AGMRGSSRRRRSEPKVRMVVVVAVLVGVGCLPFIYIVNLAFT-----LPEEPTSA 283
 Qy 291 ILYYCKEITLPLASACNVCLDPIIYFPMCRSFSRRLFKK 328

Db 284 GLYF---FVVVLSYANSCANPLLYGLSDNF-RQSFRR 317

RESULT 11

JC4162

p2y receptor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 12-Oct-1995 #sequence revision 10-Nov-1995 #text_change 24-Sep-1999

C:Accession: JC4162

R:Henderson, D.J.; Elliott, D.G.; Smith, G.M.; Webb, T.E.; Dainty, I.A.

Biochem. Biophys. Res. Commun. 212, 648-656, 1995

A:Title: Cloning and characterization of a bovine p2y receptor.

A:Reference number: JC4162; MUID:95352058; PMID:7626079

A:Accession: JC4162

A:Molecule type: mRNA

A:Residues: 1-373 <HEN>

A:Cross-references: EMBL:X87628; NID:G1032484; PIDN:CAA60958.1; PID:G1032485

A:Experimental source: aortic endothelial cell

C:Genetics:

A:Gene: bovy2y

C:Superfamily: ATP receptor P2u

C:Keywords: glycoprotein; phosphoprotein; receptor; transmembrane protein

F:52-77/Domain: transmembrane #status predicted <TM1>

F:88-111/Domain: transmembrane #status predicted <TM2>

F:124-150/Domain: transmembrane #status predicted <TM3>

F:171-191/Domain: transmembrane #status predicted <TM4>

F:214-237/Domain: transmembrane #status predicted <TM5>

F:261-282/Domain: transmembrane #status predicted <TM6>

F:305-328/Domain: transmembrane #status predicted <TM7>

F:11.27.113.197/Binding site: carbohydrate (asn) (covalent) #status predicted

F:258/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 17.4%; Score 326; DB 2; Length 373;

Best Local Similarity 25.6%; Pred. No. 1.3e-20;

Matches 87; Conservative 69; Mismatches 132; Indels 52; Gaps 9;

Qy 30 PGKNTLLHNEFDITVLPVLYLIIVASILLGLAWIF-FHIRNKTSTIFLYKNTVAVDL 88
 Db 39 PFKALTKTGQFYLLPRAVILVLIIFGLNSVAIMFVFMKPMRSGISVYMFNLADF 98
 Qy 89 IMTLFPRRIYHDAFGWYFELICRTSVLFYANMTSIVFLGLISIDRLKVKPFG 148
 Db 99 LVLTLPLALIVYFNKTDWIRGDMCKLGRIFVHNLGSLPLTCLSAHRYSGVVYDLK 158
 Qy 149 DSRKYSTITFTVLSVCVWVIMAVSLPNIITLNGQPTEDNIDGS-KLKSPLGVKMTAVT 208
 Db 159 SLGRLLKKNAAVYISLVWLIV-VGISPIILFYSG-----TGIRNKTIT 201
 Qy 209 -----YVNS-----CLFVAVLVILICGY-IAISRYIHSRQFISQSRK 249
 Db 202 CYDTTSDELYLSYITYSKCTVAMFCVPLVILICGYIGLIVALLYKD-----LNSPLRK 257
 Qy 250 HNSIRVVAVVFTCFPLPYHLCRIPFTFSLHRLDDE--SAOKILYYCKEITLPLASACNV 307
 Db 258 SIYVITIVLTVFAVSYIPFHMKTMLRLARLDFOFPCANDRVAVYATVTRGLASLNS 317
 Qy 308 CLDPIIYFPMCRSFSRRLFK-----KSNITRSSTI 338
 Db 318 CVDPILVFLAGDTFRRLSRATRKASRSRSEANLQSKSDM 357

RESULT 12

JC4737

G protein-coupled receptor P2Y1 - human

N:Alternate names: p2y1 purinergic receptor; P2Y1 purinoreceptor

C:Species: Homo sapiens (man)

C:Date: 10-May-1996 #sequence revision 16-Aug-1996 #text_change 17-Nov-2000

C:Accession: JC4737; S54253

R:Janssens, R.; Communi, D.; Pirotton, S.; Samson, M.; Parmentier, M.; Boeynaems, J.M.

Biochem. Biophys. Res. Commun. 221, 588-593, 1996

A:Title: Cloning and tissue distribution of the human P2Y1 receptor.

A:Reference number: JC4737; MUID:96205320; PMID:8630005

A:Accession: JC4737

Db 210 LSWRTMSRAYMASCPIWMLISASTIPLAVTEQTKIPRLDITTCCHVDLKD--LKDQY 266
QY 206 AVTYVNSCL--FVAVLVLLIGYIAISRYIKSSQPIISQSRKKNQSIKRVAVVPEFT 263
Db 267 IYFSSSCLLFFVFPIITTCYIGIIRSLSSS---IENSCKTKRALFLAVVLCVPII 323
QY 264 CFLPFLHLCRIPTFTSHLRLDLSAOKILYYCKEITLFLSACNVCGLDPIIYFFMCRSR 323
Db 324 CFGP---TNVLFLTYL-----QEANFLYFAYIISACVSVSCCLDPIIYYVASQQR 375
QY 324 RLFKKSNIRTRSE 336
Db 376 YLYSLCCRKVSE 388

RESULT 15

150241
G protein-coupled receptor 6H1 - chicken
N:Alternate names: purinoceptor 6H1
C:Species: Gallus gallus (chicken)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 02-Jun-2000
C:Accession: 150241; J04618
R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.
J. Immunol. 151, 628-636, 1993
A>Title: Identification of a G protein coupled receptor induced in activated T cells.
A:Reference number: 150241; MUID:93329058; PMID:8393036
A:Accession: 150241
A:Status: Preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-308 <KAP>
A:Cross-references: GB:L06109; NID:G304383; PIDN:AB06587.1; PID:G304384
R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A>Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.
A:Reference number: J04618; MUID:96190677; PMID:8619790
A:Accession: J04618
A:Molecule type: mRNA
A:Residues: 1-308 <WEB>
A:Cross-references: GB:L06109; NID:G304383; PIDN:AB06587.1; PID:G304384
A:Experimental source: T-cells
C:Comment: This receptor plays a role in T-cell activation.
C:Genetics:
A:Gene: P2Y5
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
F:15-40/Domain: transmembrane #status predicted <TM1>
F:51-74/Domain: transmembrane #status predicted <TM2>
F:89-109/Domain: transmembrane #status predicted <TM3>
F:133-153/Domain: transmembrane #status predicted <TM4>
F:177-201/Domain: transmembrane #status predicted <TM5>
F:227-248/Domain: transmembrane #status predicted <TM6>
F:269-292/Domain: transmembrane #status predicted <TM7>

Query Match 17.2% Score 321.5; DB 2; Length 308;
Best local similarity 27.7% Pred. No. 2.7e-20;
Matches 86; Conservative 67; Mismatches 135; Indels 23; Gaps 9;

QY 33 NTLTNEEDTIVLPVLYLIIFVASILNGLAVIF--FHIRNKTSFIPLYKNIVADLI 89
Db 5 NCSTEDSFXYTLVYGVFNVFLGLIANCVAIYFTFLKVRNERT--TYMLNLAIISDL 62
QY 90 MTLTFPPRIVDAGGCPWFYKILCRYTSVLFYANMTSIVFLGLISIDRYLKVYKPFQD 149
Db 63 FVFTLPFRIVYFV-VRNMPFGDVLCKISVTLFLYTNMYSILPLCTISVDRFLAIVPFRS 121
QY 150 SRMYSITFTKVLSCVWVMVAVLSLPIIL--TNGOPTEDNIDCSKLSPLGVKMT-- 205
Db 122 KTLRKRRARIYCAVMITVLAGSTPASPQSTNRQ---NNTGQRTCEPNPPESTMKTYL 178
QY 206 --AVTYVNSCLFVAVLVIIIGCYIAISRYIKS---SRQFISQSRKKNQSIKRVAV 260
Db 179 SRIVIFIEIVGFPIILNVTCSTWVLRNLKPLTLNRKLS----KKVLMIFVHLVI 234

QY 261 FFCFLPFLHLCRIPTFTSHLRLDLSAOKILYYCKEITLFLSACNVCGLDPIIYFFMCRS 320
Db 235 FCFEFVYVNTLILYSIMRQGTWINCSVYAVRMYPVTLCIAVSNCCFDBIVYFTSDT 294
QY 321 FSRRLFKKSNIR 331
Db 295 NS-ELDKKQGV 304

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Job time : 21 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:13:50 ; Search time 45 Seconds
(Without alignments)
2510.123 Million cell updates/sec

Title: US-09-464-685-1
1674

Perfect score: 1 MGFNUTLAKLPNNELHGOES.....RSLQSVRSEVRITYDTDV 358

Sequence: 1 MGFNUTLAKLPNNELHGOES.....RSLQSVRSEVRITYDTDV 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioid:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	768.5	41.0	338	4	Q81YT7
2	692	36.9	347	11	Q8BZV8
3	683.5	36.5	342	6	Q8BXH1
4	423	22.6	319	11	Q8C1F3
5	422	22.5	319	11	Q8BGS5
6	419.5	22.4	319	4	Q81V06
7	419	22.4	319	11	Q8BY85
8	417	22.3	317	11	Q8BTN1
9	381.5	20.4	309	11	Q8RS28
10	374	20.0	374	13	Q57466
11	369	19.7	375	11	Q8BYT1
12	369	19.7	376	4	Q723M3
13	368.5	19.7	347	13	Q72ZK4
14	355	18.9	339	4	Q8N577
15	352	18.8	537	13	Q72M07
16	351.5	18.8	358	13	Q72XJ7

17	350.5	18.7	357	11	Q7TMV7	Q7TMV7 mus musculus
18	350.5	18.7	358	13	Q9YGC3	Q9YGC3 xenopus lae
19	348	18.6	399	11	Q8R311	Q8R311 mus musculus
20	347.5	18.5	341	11	Q8C017	Q8C017 mus musculus
21	347	18.5	353	13	Q93247	Q93247 cypinus ca
22	346	18.5	357	13	Q9DB05	Q9DB05 raja erinac
23	339	18.1	342	6	Q9TTY5	Q9TTY5 bos taurus
24	334.5	17.8	354	13	Q7ZM0	Q7ZM0 xenopus lae
25	334	17.8	337	4	Q81V19	Q81V19 homo sapien
26	332	17.7	342	6	Q9GK76	Q9GK76 capra hircu
27	332	17.7	353	13	Q9PFR7	Q9PFR7 brachydanio
28	330.5	17.6	358	13	Q9DC11	Q9DC11 gallus gall
29	330.5	17.6	369	11	Q8BJ87	Q8BJ87 mus musculus
30	328.5	17.6	361	11	Q8VMP3	Q8VMP3 cavia porce
31	328.5	17.4	176	4	Q9BY61	Q9BY61 homo sapien
32	326.5	17.4	390	13	Q8QG04	Q8QG04 carassius a
33	325.5	17.4	352	6	Q7YS92	Q7YS92 tupia bela
34	324	17.3	349	11	Q8VD47	Q8VD47 rattus norv
35	324	17.3	359	13	Q9PVY7	Q9PVY7 anguilla an
36	323.5	17.3	342	6	Q9XSD4	Q9XSD4 sus scrofa
37	323.5	17.3	347	6	Q9MZM9	Q9MZM9 steles pani
38	323.5	17.3	358	13	Q9PUA0	Q9PUA0 acipenser r
39	322.5	17.2	334	6	Q9N130	Q9N130 salmiki bol
40	322.5	17.2	347	6	Q9MZM7	Q9MZM7 callimico g
41	322	17.2	373	11	Q8BMU5	Q8BMU5 mus musculus
42	321	17.1	296	6	Q9TY6	Q9TY6 canis famli
43	320.5	17.1	334	6	Q9N1P3	Q9N1P3 hylobates l
44	320.5	17.1	347	6	Q9MZN6	Q9MZN6 hylobates c
45	320.5	17.1	347	6	Q9MZN5	Q9MZN5 hylobates h

ALIGNMENTS

RESULT 1
ID Q81YT7 PRELIMINARY; PRT; 338 AA.

NC Q81YT7
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE G protein-coupled receptor 105.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034989; AAH34989.1; -
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0004872; F:Receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR005466; UDPG_Receptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCRHOOPS.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS50262; G_PROTEIN_RECPE_F1_2; 1.
KW Receptor.
SQ SEQUENCE 338 AA; 38972 MW; 88714082F32DEB CRC64;

Query Match 41.0%; Score 768.5; DB 4; Length 338;
Best Local Similarity 47.6%; Pred. No. 1.1e-58;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

QY 44 VLPLVLIIFVASYLNLGLAVWIFPHIRNKTSFTFYLNKIYVADLIIMLTTPPRFVHDAG 103
DB 24 IIPLVYCWVFIAGILNLSGVSMIFPVYSSSFIIYLNIVADVFWMSLTPEPKLIDSG 83

[illegible]

	RESULT 2
QBZV8	ID
AC	QBZV8; PRELIMINARY; PRT; 347 AA.
DT	01-MAR-2003 (TrEMBLrel. 23, Created)
DT	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	P2Y12 platelet ADP receptor homolog.
GN	P2RY12
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX	NCB1_Taxid=109090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=C57BL/6J; TISSUE=Colon;
RC	MEDLINE=22354683; PubMed=12466651;
RA	The FANTOM Consortium,
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;
RT	"Analysis of the mouse transcriptome based on functional annotation of
RT	60,770 full-length cDNAs."
RL	Nature 420:563-573 (2002) .
RL	EMBL: AK033448; BMC28294.1; -.
DR	MCD; MG1:1818089; P2ry12.
DR	GO; GO:0005887; C:integral to plasma membrane; IC.
DR	GO; GO:0001609; G:adenosine receptor activity; G-protein coupled; IMP.
DR	GO; GO:0001623; P:platelet ADP receptor activity; IMP.
DR	GO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. . .; IMP.
DR	GO; GO:0030168; P:platelet activation; IMP.
DR	InterPro: IPRO00276; GPCR Rhodpsn.
DR	InterPro: IPRO05394; P2Y12_purinocptor.
DR	pfam: PF00001; 7cm_1.1.
DR	PRINTS: PR00237; GPCRRHODPSN.
DR	PRINTS: PRO1569; P2Y12PRINCEPTR.
DR	PROSITE: PS00262; G_PROTEIN_RESCP_F1_2; 1.
SQ	SEQUENCE 347 AA; 39430 MW; F1468837FE25F1 CRC64;
	Query Match 36.9%; Score 692; DB 11; Length 347;
	Best Local Similarity 43.3%; Pred. No. 4.9e-52;
	Matches 136; Conservative 60; Mismatches 102; Indels 16; Gaps 2;
QY	28 DPGKNTLLHN-----BEDTIVLPVLIIIFVASILLNGIAWIFEHHRN 72
DB	2 DYFGVNTTSANTTSPSGISTLCRADYKITOVLPFLTYLVFGLITNSLARIFPOIRS 61
QY	73 KTSFIIFYKNIVADLTIMTLTFPPRIVDAGFGPWFKFTLCRYTSVLFFAMYSIYEL 132
DB	62 KSNFIIFPKNTVIIDLIMILTFPKLIDAKLGAPLRTLVCQVSIVTFYFMYSISFL 121
QY	133 GLISIDRLTKVKRFGDSRMATSIFFTVLSVCWVMVAULSLPNITLTNGQPTEDNIHC 192
DB	122 GLITIDRLTKTRPFKSTSSPNILGAATISVVIAWFPIISLPNNMLITNRBKDDVTKC 181

[illegible]

RESULT 3		
08HXH1		
ID	PRELIMINARY;	PRT, 342 AA.
AC	08HXH1;	
DT	01-MAR-2003 (TREMBLrel. 23, Created)	
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE	Hypotheetical protein.	
OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;	
OC	Cercopithecinae; Macaca.	
OX	NCBI_TaxID=9541;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Medulla oblongata;	
RA	Hashimoto K., Osada N., Hida M., Kusunagi J., Sugano S.;	
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.	

RP SEQUENCE FROM N.A.
RC TISSUE=Medulla oblongata;
RX MEDLINE=21458551; PubMed=11574149;
RA Oseada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
RR Hirata M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;
RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human
RL chromosomes.";
DR Gene 275:31-37 (2001).
DR EMBL, AB097554; BAC14779.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0045028; F:purinergic nucleotide receptor activity; G-. .; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR InterPro; IPR005394; P2Y12_purinocptor.
DR Pfam; PF00001; Tcm.1; 1.
DR PRINTS; PR00237; GPCRHRHODPSN.
DR PRINTS; PR01569; P2Y12PRNCPTP.
DR PROSITE; PS50262; G_PROTEIN_RECEP_FL_2, 1.
KW Hypothetical protein.
KW SEQUENCE 342 AA; 39479 MW; 0869FDD0144A56FC CRC64;

[illegible]

Db 185 VMHEIVNYICQVSIWNIPLIVCYTLITLKEIYRSYVTRGVKVPK-KVNVKVFIIIA 243
Qy 260 VFFTCFLPYHLCRIPFTSHDLDESAOKILYYCKEITLPLSACNCLDPIIYFPCGR 319
Db 244 VFFTCFVPHARIPYTLISQTRDVPDCAENTLFFVCKESTLMLSLACLDPIYFLCK 303
Qy 320 SFSRRLPKKSNIRTSISIRLSQVRSE 348
Db 304 SFRNSLI--SMLKCPNSATSSQDNKKE 330

RESULT 4

08CIF3 PRELIMINARY; PRT; 319 AA.
AC 08CIF3
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to platelet activating receptor homolog.
GN F73000IG1SRK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II;
RA Straubeberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024054; AAH24054.1; -
DR MGD; MGI:2442043; F73000IG1SRK.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
KW Receptor.
SQ SEQUENCE 319 AA; 36705 MW; 11E0D6556B694361 CRC64;

Query Match 22.6%; Score 423; DB 11; Length 319;
Best Local Similarity 30.9%; Pred. No. 1e-28; Indels 16; Gaps 5;
Matches 93; Conservative 63; Mismatches 129;

Qy 49 YLIIFVASILNGLAWIFPH-IRNKTSPFYLNKIIVADLIMLTFFPRIVHDAGFGPW 107
Db 21 FYLVFLIGIISCFATMAFIQKTNHRCVSIVLINLADPLTLALPVKIIVDIGVAPW 80
Qy 108 YFKFLCYTSVLFANNMTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVAV 167
Db 81 KLRIFFCQVTAACLIYNNMYSIIPLAFVSDICQLHISCKIYRQEGFAMISAIVWL 140
Qy 168 IMAVLSLENIITNGOPTEDNIHDSKSLSPGVGMHTAVTVVNSCLFAVAV-LVILIGCY 226
Db 141 MVLIMVNMVYIPIKDIKESNVGMEPEKFGRMHLLTNFICVAIFLNFSVIILLISNF 200
Qy 227 IAIISR-YIHKSROFISQSSRRKKNOSIRVVAVFFTCFLPYHLCRIPFTSHDLRLD 285
Db 201 LAIRQLYNNRNTNTPSVKSL-----LHLLLVTAAYIICFVPHAVRIPYTLISQTEVSD 256
Qy 286 ESAOKILYYCKEITLPLSACNCLDPIIYFPCGRSF-----SRRLPKKSNIRTSSE 336
Db 257 CSTRIALPKAKEATLLAVSNLCFDPILYHLSKAFRLKVTETPASPCKSKPLERLASE 316
Qy 337 S 337
Db 317 N 317

RESULT 5

08BG55 PRELIMINARY; PRT; 319 AA.
ID 08BG55
AC 08BG55
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Probable G protein-coupled receptor H963 homolog.
GN F73000IG1SRK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs".
RL Nature 420:563-573(2002).
DR EMBL; AK041381; BAC10925.1; -
DR EMBL; AK089287; BAC40829.1; -
DR MGD; MGI:2442043; F73000IG1SRK.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPT_F1_2; 1.
SQ SEQUENCE 319 AA; 36719 MW; CE50D58FB694364 CRC64;

Query Match 22.5%; Score 422; DB 11; Length 319;
Best Local Similarity 30.6%; Pred. No. 1.3e-28;
Matches 92; Conservative 64; Mismatches 129; Indels 16; Gaps 5;

Qy 49 YLIIFVASILNGLAWIFPH-IRNKTSPFYLNKIIVADLIMLTFFPRIVHDAGFGPW 107
Db 21 FYLVFLIGIISCFATMAFIQKTNHRCVSIVLINLADPLTLALPVKIIVDIGVAPW 80
Qy 108 YFKFLCYTSVLFANNMTSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVAV 167
Db 81 KLRIFFCQVTAACLIYNNMYSIIPLAFVSDICQLHISCKIYRQEGFAMISAIVWL 140
Qy 168 IMAVLSLENIITNGOPTEDNIHDSKSLSPGVGMHTAVTVVNSCLFAVAV-LVILIGCY 226
Db 141 MVLIMVNMVYIPIKDIKESNVGMEPEKFGRMHLLTNFICVAIFLNFSVIILLISNF 200
Qy 227 IAIISR-YIHKSROFISQSSRRKKNOSIRVVAVFFTCFLPYHLCRIPFTSHDLRLD 285
Db 201 LAIRQLYNNRNTNTPSVKSL-----LHLLLVTAAYIICFVPHAVRIPYTLISQTEVSD 256
Qy 286 ESAOKILYYCKEITLPLSACNCLDPIIYFPCGRSF-----SRRLPKKSNIRTSSE 336
Db 257 CSTRIALPKAKEATLLAVSNLCFDPILYHLSKAFRLKVTETPASPCKSKPLERLASE 316
Qy 337 S 337
Db 317 N 317

RESULT 6

08IV06 PRELIMINARY; PRT; 319 AA.
ID 08IV06
AC 08IV06
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Platelet activating receptor homolog.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;


```

Qy 49 YLIFVAILNGLAWIFPHIRNKTSIFLYKNIIVADLIMTLTPPRIVHDAFGPMY 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 21 FYLVFLIGIIGSCPTMA-FKTTNRCVSYIYINLTADFLITLPAKTIIDLGVAHWK 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 109 FKFLICRYTVLFPYANMTYSIVFLGLISIDRYLKYVKGDSRWYSITFTKLVSCWVI 168
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 80 LRFHCQVLAELIYINMTYSITFLAFVSDIRCLQIHSCIKYRIQEPGAKMISAVWLM 139
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 169 MAVLSLPIIILNGPTEDNIDHCKSLSPGVKHTAVTVNSCLFPAV-LVILIGCI 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 140 VLLIMVPMMAIPIDIKERSNVGCFKKEFGRNHLLTNFLCVALFINFSVILISNPL 199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 228 AISR-YIKHSRQFISQSRKKNQSIKRVVAVFPTCELPYHLCRIPFTSHLDRLDE 286
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 200 AIRQIYRNRDNTNYSVKSAL----LHLLVYASITICFVPHAVRIPITLSQTEVISDC 255
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 287 SAOKILVYCKEITLPLSACNVCLDPIYFMCGRSF-----SRLLFKSNIRTRSES 337
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 256 STRIALPFAKEATLLAVSNLCFDPILYVHLSKAFRLKVTETPAAPKSKPLEERLSEN 315
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 9

Q8R528 PRELIMINARY; PRT; 309 AA.

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ID 08R528;
AC Q8R528;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Cytelrhny1 leukotriene 2 receptor.
GN CysLR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
   [1]
RN RP
   SEQUENCE FROM N.A.
RA Ishii S.;
RT Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; AB058930; BAB86881.1; -.
DR MGI; MGI:1917336; CysLR2.
DR GO; GO:0001631; F:cytelrhny1 leukotriene receptor activity; IDA.
DR InterPro; IPR004071; Cyaleuk receptor.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO1533; CysLTRRECPTR.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 309 AA; 35226 MW; 96FACC6B8AF96974 CRC64;

```

Query Match 20.4%; Score 381.5; DB 11; Length 309;
 Best Local Similarity 31.5%; Pred. No. 4e-25;
 Matches 102; Conservative 56; Mismatches 133; Indels 33; Gaps 12;

```

Qy 23 SGNRDGGCKNTLNEPTIVLPVLYLIIFVASILNGLAWIFPH-IRNKTSTIFYLK 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 TGPSSYSNRCTIN-FKKEFYPIIYLIIFWGAIGNGFSIYVLTQCTCKSTSVNFMFL 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 82 NIVVADLIMTLTPPRIVHDAFGPMYFKFLICRYTVLFPYANMTYSIVFLGLISIDRYL 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 63 NLATSDPLFISTLPRADYIFRGSNMIFGDLACRWMSLSLYNMWTSITFLTVLSVAFPL 122
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 142 KVVKFGDSRWYSITFTK--VLSVCWVIMAVLSLPIIILNGPTEDNIDHC-----S 193
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 123 ATVHPF--RMFHTVSVSAMILGIIWVF--IMASSALLVNGGEEKNIISCLELSPQ 177
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 194 KLSKSLGVKMTAVYVNSCLFPAVAVLILIGCIYASIRYIHKSROFISQSRKKNQ 253
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 KFKSL-LIMNHAV---AVGFLPLPFLITTCYLLIRLLAB--IPESGPRAAHKA 229
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 254 IRVVV---AVFPTCELPYHLCRIPFTSHLDRLDESAOKILVYCKEITLPLSACNVCLD 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

Db 230 LTTIVAMITFLCFLPYHALRT----LHLYVWDRKSGDVLKATVITLTAANSNGFN 285
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 311 PIIFYFMCRSFRLL---FKSKNI 331
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 PFLYYFAGENFKARLALFSLVHL 309
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10

057466 PRELIMINARY; PRT; 374 AA.

```

ID 057466;
AC 057466;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE G protein coupled p2y nucleotide receptor.
GN TP21.
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
   [1]
RN RP
   SEQUENCE FROM N.A.
RA TISSUE=Blood;
RX MEDLINE=98086419; PubMed=9415702;
RA Boyer J.L., Waldo G.L., Harden T.K.;
RT "Molecular cloning and expression of an avian G protein-coupled p2y
   receptor."
RL Mol. Pharmacol. 52:928-934(1997).
DR EMBL; AF031897; AAC60339.1; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signaln. . .; IEA.
DR InterPro; IPR00276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PRO0237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECPEP_FL_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECPEP_FL_2; 1.
KW Receptor.
SQ SEQUENCE 374 AA; 42594 MW; 849C465722BDD02B CRC64;

```

Query Match 20.0%; Score 374; DB 13; Length 374;
 Best Local Similarity 29.3%; Pred. No. 2.2e-24;
 Matches 95; Conservative 67; Mismatches 132; Indels 30; Gaps 9;

```

Qy 31 GNNT-----LHNEFDIVLPVLYLIIFVASILNGLAWIFPH-IRNKTSTIFYLK 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 GNTTAAAEAKCVNEEFKFLIPISYGVFVGLPLNSMAMWIFVSRMRPNVATTVWF 81
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 82 NIVVADLIMTLTPPRIVHDAFGPMYFKFLICRYTVLFPYANMTYSIVFLGLISIDRYL 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 NLATSDPLFISTLPRADYIFRGSNMIFGDLACRWMSLSLYNMWTSITFLTVLSVAFPL 141
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 142 KVVKFGDSRWYSITFTK--VLSVCWVIMAVLSLPIIILNGPTEDNIDHCKSLSP 199
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 GICHPISLKVYKTHARLICGVWLVVTICLIPILIVTSSKNSKNSLCHDTTPB--- 198
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 200 GVKHTAVTVNS---CLFPAVAVLILIGCIYASIRYIHKSROFISQSR---RKHNQ 252
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 199 --EFDHVHYASSIMALLFGIPFLIVIVCYCLMARLCK--RSFSPSPRPVSVYKRSIK 254
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 253 SIRVVAVFPTCELPYHLCRIPFTSHLDRLDESAO--KILYCKEITLPLSACNVCLD 310
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 255 MIITLVTFALCPVEFHTR--TLVYSRYFQADCOPLNIINFTYKILTRPLASINSCLD 311
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 311 PIIFYFMCRSFRRLFKSNIRTR 334
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 312 PLYVFMADKXRGRLRGAQRPR 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 11

08BY11 PRELIMINARY; PRT; 375 AA.

AC 08BY11; (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Wamburt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
 RA Robo G., Han M., Wiemann S.,
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BX517386; CAD97628.1; -
 DR EMBL: BX517386; CAD97628.1; -
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 376 AA; 42720 MW; 7638373C15A695DD CRC64;
 Query Match 19.7%; Score 369; DB 11; Length 376;
 Best Local Similarity 29.6%; Pred. No. 5.9e-24;
 Matches 102; Conservative 63; Mismatches 148; Indels 32; Gaps 10;
 16 HGSEHNSGNRSDGPGKNTT-----LNHEPDTVLPLVLIIFVASTILNGLAWI 66
 14 HCM-HFTVNSDQSQNFGVNPVTSCEPDEKLTSTVLTFFYSVIFVGLVGNILAV 71
 67 FPH-RNKTSTFIYKNIIVADLIMLTFFPIVDAGGPGYFFILCRYTVLFFYANM 125
 72 FGIHRKNSIQIYILNANVADLILFCLPFRIMYHINONKNTLGVILCKVGLTFYANM 131
 126 YTSIVFLGLISDRYLKVKVFGDSRWSTTFEVLVSV--VWIMAVLSLPIILLT--- 180
 132 YTSIILGFIISDRYIKIRSIQGR-AITTKQSIYVCIWTVVLAAGFLMILHLTK 189
 181 NQOPTEDNHDCSKLSPGVKMTAVTVYNSCLFVAVVILIGCTAISRVIHK--SSR 238
 190 GGH---NSTMCFHYDRNKAKEAIFNFVLMVWMLIFLILISYIKIKKILRIPKR 245
 239 QFISQSRKKNQSRVVAVFPCFLPYHLCRIPTFSHLDLDESA---OKILYYC 295
 246 SKFNSCKYATYANSEFVILITFCFVYH---AFRFIYISSQLNNSCQKEIHK 301
 296 KEITFLSACNVCLDPIIYFFMCRSFRRLFKKSNIRTSSESIR 340
 302 NEIMLVSSFNSCIDPVWYFLMSNIRKIMCOLLFRPFSERS 346
 RESULT 12
 0723W3 PRELIMINARY; PRT; 376 AA.
 AC 0723W3;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein DKFZ686N1782.
 GN DKFZ686N1782.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catartini; Homidae; Homo.
 NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.
 RC TISSUE=Human retina;
 RA Wamburt R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
 RA Robo G., Han M., Wiemann S.,
 RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: BX517386; CAD97628.1; -
 DR EMBL: BX517386; CAD97628.1; -
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 376 AA; 42720 MW; 7638373C15A695DD CRC64;
 Query Match 19.7%; Score 369; DB 11; Length 376;
 Best Local Similarity 28.6%; Pred. No. 5.9e-24;
 Matches 94; Conservative 65; Mismatches 122; Indels 48; Gaps 10;
 32 KNTT---LNHEPDTVLPLVLIIFVASTILNGLAWI-IFPHIRNKTSTFIYKNIIVAD 87
 81 KNTMGVLTSSLSSTKILPAIYLVFVGVNPNVATLWMLFFRTSISCTTVY-TNLALD 139
 88 LMTLPPFPRIVDAGFGVYKFLCRYTVLFPANNYSIVFLGISDRYLKVKRP 147
 140 FLFCVTLFPIKXANHLNNGNMFGEVLCRAVTVIFGNWICSLILLACISINRYLATVHP 199
 148 GDSRWYSITFTKVLSSCVWIMAVLSLPIILLTNG---QP---TEDNHDCSKLSPFG 200
 200 TYRGLPKHTVALVYGLVWATVFLWMLPFIKQEVYVOPDITTCVHNATCSSSPFQ 259
 201 VKMHTAVVYNSCLFVAVVILIGCTAISRVIHSSRFISQSRKKNQSRVVAV 260
 260 LYFISLAFPG--FLIPFVLIIYCAAIRILNADHML-----WYVASTLILVI 309
 261 FTTCFLPYHLCRI---PFTSHLDRLDLSAOKILYCKEITLPLSACNVCLDPIIYFF 316
 310 FTICFAPSNIILIIHNAVYNNMDG-----LYFVILMLCIGLSNCLDPLVYL 360
 317 MCRSFRRLFKKSNIRTSSESIRLSQVR 345
 361 MS-----KTRNHSYATLITVK 376
 RESULT 13
 0722A4 PRELIMINARY; PRT; 347 AA.
 ID 0722A4;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE SI:B24632.9 (Novel protein similar to nucleotide receptors).
 GN SI:B24632.9 (zebrafish) (Danio rerio).
 OS Brachydanio rerio (zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 NCBI_Taxid=7955;
 RP SEQUENCE FROM N.A.
 RA Skuce C.;
 RA Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
 RL EMBL: AL590151; CAD68067.1; -
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0004872; F: receptor activity; IEA.
 DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P: G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 347 AA; 39861 MW; 3D3C01F93CC283E2 CRC64;
 Query Match 19.7%; Score 368.5; DB 13; Length 347;
 Best Local Similarity 31.0%; Pred. No. 6.1e-24;
 Matches 99; Conservative 62; Mismatches 127; Indels 31; Gaps 11;

```
QY 35 TLHNEPDTIV.PVLYLIFVASILLNGLAWIIF-HIRNKTSFIYLNIVADLIMLT 93
DB 13 TFDSEFKILLPVSLVCLPFGILLNSVALMMFTTKMPKSTVYVHMLSDLYLVS 72
QY 94 PPRIVHDAGFGPMYFKELICRYTSVLFYANMTYSIVELGLISIDRYLKVVKPFGDSRMV 153
DB 73 LPMIYYAANSNHPFGVVLCKIVRFLFYANLYCSILFLTGISVRYGICHF-----IR 127
QY 154 SITPTK--VLSVC--VWVIAVLSLENIILITNGOPTEDN--HDCSLKSPILGVKHTA 206
DB 128 SLTLIKPRHAMWCGFVTAIVACLPVTLVNTSRNNSITLCHDTSRPE-----EFHNF 182
QY 207 VTY---VNSCLFVAVLVILIGCYIAISRYIHKSROFI--SOSRKRKNGSIRVVAVF 261
DB 183 VTNSSVWVWLFIPLFELVIVCYCLMARALCOPKRGALANQOSSSRKSKITLIVLVLF 242
QY 262 PTCFLPYNLICRIPFTSHDLRLDESAC--KILYYCKEITLFLSACVCLDPIIYFVW-- 317
DB 243 AICVPPHITR---TLVYVRIFPADCKTLNIVNSYKITRPLASVNSCLDPIIYFLAGD 299
QY 318 -CRSPSRRLFKKSNIRTS 335
DB 300 HYRSKLRVLTRQTPNTRS 318

RESULT 14
Q8NS57 PRELIMINARY; PRT; 339 AA.
AC Q8NS57;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE G protein-coupled receptor 17.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Primates; Catarrhini; Homiidae; Homo.
-XX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, and Lung;
RA Strauberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC031653; AAH31653.1; -.
DR GO: GO:0016021; C:Integral to membrane, IEA.
DR GO: GO:0004872; F:receptor activity, IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity, IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 339 AA; 37860 MW; BBGCAFD0FC371D63 CRC64;

Query Match 18.9%; Score 355; DB 4; Length 339;
Best Local Similarity 30.2%; Pred. No. 8.8e-23;
Matches 95; Conservative 46; Mismatches 124; Indels 50; Gaps 8;

QY 31 GKNTLHNEPDTIV.PVLYLIFVASILLNGLAWIIFH-IRNKTSFIYLNIVADLI 89
DB 24 GQETPLER---MLPASFLYLDLFIATVGNLTALMFLRDKSGTPRANVFLMHLAVDLS 79
QY 90 MTLTPPRIVHDAGFGPMYFKELICRYTSVLFYANMTYSIVELGLISIDRYLKVVKPFGD 149
DB 80 CVLVLPTRLVVHFGSNHMPFGELICRLTGLFLFYLMVMSIYFLTGISADRFALVHPYKS 139
QY 150 SRMTSITTKVLSVCVWVIAVLSLENIILITNGOPTEDNHDSCSLKSPILGVKHTAVTY 209
DB 140 LKLRRLPVLAHLCALFLWVAVVAVAMAP--LVSPQTVQTN-----HTVV-- 180
QY 210 VNSCL-----FAVALVILIGCYIAISRYIHKSROFISOSSR-KKKH 250
```

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DB 181 ---CLQYREKASHNALVSLAVAFTPRITVTCYLLIR-----SLRGLNREKSLKTKKA 233
QY 251 NQSRIVVAVVFFCPFLPYNLICRIPFTSHDLRLDESACQILYYCKEITLFLSACVCLD 310
DB 234 VRMIATVIAFLVCFVPPHVRVRSYVVLHYRSHGASCATQRIALANLRITSLTSLNGALD 293
QY 311 PIIFYPMCRSPSRRL 325
DB 294 PIMTFVAKERFHAL 308

RESULT 15
Q7ZMO7 PRELIMINARY; PRT; 537 AA.
AC Q7ZMO7;
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
-XX NCBI_TaxId=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strauberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC046837; AAH46837.1; -.
DR GO: GO:0016021; C:Integral to membrane, IEA.
DR GO: GO:0001584; F:rhodopsin-like receptor activity, IEA.
DR GO: GO:0007186; P:G-protein coupled receptor protein signaln. .; IEA.
DR Interpro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PR00237; GPCR_RHODOPSIN.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 537 AA; 61981 MW; B030F67D76CB9622 CRC64;

Query Match 18.8%; Score 352; DB 13; Length 537;
Best Local Similarity 31.0%; Pred. No. 2.5e-22;
Matches 95; Conservative 58; Mismatches 133; Indels 20; Gaps 10;

QY 40 FDTIVLPVLYLIFVASILLNGLAWIIF-HIRNKTSFIYLNIVADLIMLTLPFPR 98
DB 41 FKPLLPVSAVAVMVGPLNIAAMWIFIAKGRPMNPPTVYVNFNLASDLYVLSLPLV 100
QY 99 VHDAGFGPMYFKELICRYTSVLFYANMTYSIVELGLISIDRYLKVVKPFGDSRMVSTFT 158
DB 101 YVYADKNMMPGVELICLVRLFYANLYSSILFLTGISVHRYGVCHEPITSLRRNACGA 160
QY 159 KVLSCVWVIAVLSLENIILITNGOPTEDN--HDCSLKSPILGVKHTAVTVNSCLF 215
DB 161 VVICALWLSSTLGLVNLIVTVSPKKRATICHDTTRBPAPKAVETSTAL----KLL 216
QY 216 VAV-LVLIGCYIAISRYHK--SSROFISQSRKRKNGSIRVVAVFFTCFLPYNLIC 271
DB 217 FGICLLIAGCYGAMTEBLKMPVYSNGOQLPSYKSKSIKTIIFMMLA-FAICFMPHIT 275
QY 272 RIPTFSHDLRLDES--AQKILYYCKEITLFLSACVCLDPIIYFPMCRSPSRRLFKS 329
DB 276 R---TLVYVRIALDKCYALNVIVVTVKTRPLASNSCIDPIIYFLANDRYRRLIR-- 330
QY 330 NITRS 335
DB 331 TVRRRS 336

Search completed: June 1, 2004, 15:18:43
Job time : 47 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:13:14 ; Search time 17 Seconds

(without alignments)
1096.536 Million cell updates/sec

Title: US-09-464-685-1

Perfect score: 1874

Sequence: 1 MGNPLTLAKLNENELHGOES.....RSLQSVRSVRVRYDYTDV 358

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Swissprot_42:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1874	100.0	358	1	GP87_HUMAN
2	1731	92.4	358	1	GP87_MOUSE
3	768.5	41.0	338	1	P2YX_HUMAN
4	742.5	39.6	338	1	P2YX_MOUSE
5	700.5	37.4	343	1	P2YC_HUMAN
6	696	37.1	342	1	P2YC_MOUSE
7	694.5	37.1	342	1	GP86_HUMAN
8	692.5	37.0	333	1	GP86_MOUSE
9	686.5	36.6	342	1	P2YC_MOUSE
10	672.5	35.9	305	1	P2YX_MOUSE
11	666	35.5	337	1	GP86_MOUSE
12	491.5	26.2	245	1	GP86_MOUSE
13	420.5	22.4	319	1	H963_HUMAN
14	376.5	20.1	309	1	CLT2_MOUSE
15	375.5	20.0	342	1	P2YC_MOUSE
16	374	20.0	375	1	GP34_MOUSE
17	372.5	19.9	345	1	CLT2_MOUSE
18	371.5	19.8	381	1	GP34_MOUSE
19	370	19.7	346	1	CLT2_MOUSE
20	368.5	19.7	374	1	GP34_MOUSE
21	360	19.2	341	1	P2YX_MOUSE
22	359.5	19.2	309	1	GP86_MOUSE
23	358	19.1	367	1	GP17_MOUSE
24	356.5	19.0	341	1	P2YX_MOUSE
25	356.5	19.0	397	1	P2YX_MOUSE
26	354.5	18.9	368	1	P2YX_MOUSE
27	352	18.8	537	1	P2YX_MOUSE
28	349.5	18.6	361	1	P2YX_MOUSE
29	349	18.6	365	1	P2YX_MOUSE
30	348.5	18.5	397	1	P2YX_MOUSE
31	346	18.5	397	1	P2YX_MOUSE
32	345	18.4	361	1	P2YX_MOUSE
33	345	18.4	361	1	P2YX_MOUSE

34	343.5	18.3	361	1	P2YX_MOUSE	Q91877 mus musculus
35	340.5	18.2	342	1	P2YX_MOUSE	P25105 mus musculus
36	339.5	18.1	340	1	CLT1_MOUSE	O95002 sus scrofa
37	334	17.8	337	1	CLT1_MOUSE	Q91271 mus musculus
38	333.5	17.8	369	1	P2YX_MOUSE	O08675 mus musculus
39	330.5	17.6	339	1	CLT1_MOUSE	Q92478 mus musculus
40	330	17.6	373	1	P2YX_MOUSE	P49651 mus musculus
41	329.5	17.6	362	1	P2YX_MOUSE	P49652 mus musculus
42	329	17.6	373	1	P2YX_MOUSE	P59902 mus musculus
43	328	17.5	362	1	P2YX_MOUSE	P44996 mus musculus
44	328	17.5	377	1	P2YX_MOUSE	P41231 mus musculus
45	327	17.4	363	1	SSRS_MOUSE	P30938 mus musculus

ALIGNMENTS

ID	GP87_HUMAN	STANDARD	PRT	358 AA
AC	Q9B21, Q9B28, Q9BXC2			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Probable G protein-coupled receptor GPR87.			
GN	GP87 OR GPR95 OR FKSG78.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
NC	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21172992; PubMed=11273702;			
RT	Wittenberger T., Schaller H.C., Heilbrand S.;			
RT	"An expressed sequence tag (EST) data mining strategy succeeding in			
RT	the discovery of new G-protein coupled receptors.";			
RL	J. Mol. Biol. 307:799-813(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21458557; PubMed=11574155;			
RA	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhiko O.;			
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;			
RT	"Discovery and mapping of ten novel G protein-coupled receptor			
RT	gene 275-83-91(2001).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Isoqai T., Ota T., Hayashi K., Sugiyama T., Otaki T., Suzuki Y.;			
RA	Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.;			
RA	Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.;			
RA	Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.;			
RA	Watanabe S., Kimura K., Murakami K., Ishi S., Kawai Y., Saito K.;			
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.;			
RA	Ninomiya K., Iwayanagi T.;			
RT	"NEO human cDNA sequencing project.";			
RT	Submitted (MAY-2001) to the EMBL/Genbank/DBJ databases.			
RL	[4]			
RP	SEQUENCE OF 13-358 FROM N.A.			
RC	TISSUE=Heart;			
RA	Wang Y.-G., Gong L.;			
RT	"Identification of FKSG78, a novel gene encoding a putative G-protein-			
RT	coupled receptor.";			
RT	Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.			
RL	[5]			
RP	SEQUENCE OF 66-358 FROM N.A.			
RC	TISSUE=Lung;			
RA	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.;			
RA	Klausner R.D., Collins F.S., Wagner L., Schein C.M., Schuler G.D.;			
RA	Altshuler S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.;			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.;			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.;			

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Tohbiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Lonnell N.A., Peters G.U., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.R., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting J., Halton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Schnerker A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in placenta and prostate. Weaker
 CC expression in thymus. Not expressed in thalamus, hippocampus, pons
 CC or cerebellum.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC
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 CC
 CC EMBL: AF237763; AAK01858.1; -;
 CC EMBL: AF411114; AAL26485.1; -;
 CC EMBL: AK027784; BAB53366.1; -;
 CC EMBL: AF345566; AAK29069.1; -;
 CC EMBL: BC009540; AAH09540.1; ALT_INIT.
 CC MIM: 606379; -;
 CC GO: GO:0016021; C: integral to membrane; NAS.
 CC GO: GO:0016526; F: G-protein coupled receptor activity; unknown. .; NAS.
 CC InterPro: IPR000276; GPCR Rhodopsin.
 CC InterPro: IPR008109; P2Y13_purinocor.
 CC Pfam: PF00001; 7tm.1; 1.
 CC PRINTS: PR00237; GPCRHOOPEN.
 CC PRINTS: PR01735; P2Y13PRNCPTR.
 CC PROSITE: PS00237; G PROTEIN RECEPTOR FL 1; 1.
 CC PROSITE: PS50262; G PROTEIN RECEPTOR FL 2; 1.
 CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 CC FT DOMAIN 1 47
 CC FT TRANSMEM 48 68
 CC FT DOMAIN 69 75
 CC FT TRANSMEM 76 96
 CC FT DOMAIN 97 116
 CC FT TRANSMEM 117 137
 CC FT DOMAIN 138 159
 CC FT TRANSMEM 160 180
 CC FT DOMAIN 181 208
 CC FT TRANSMEM 209 229
 CC FT DOMAIN 230 256
 CC FT TRANSMEM 257 277
 CC FT DOMAIN 278 297
 CC FT TRANSMEM 298 318
 CC FT DOMAIN 319 358
 CC FT DISULFID 114 192
 CC FT CARBOHYD 4 4
 CC FT CARBOHYD 25 25
 CC FT CARBOHYD 33 33
 CC FT CONFLICT 154 154
 CC FT SEQUENCE 358 AA, 41445 MW, FDI157295BES10F CRC64;
 CC
 CC Query Match 100.0%; Score 1874; DB 1; Length 358;
 CC Best Local Similarity 100.0%; Pred. No. 7.9e-116;
 CC Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 MGNFUTLAKLPNNELHGOESHNSGKRSOPGKNTTLHNEFDITLVPYLIIIFVASILLN 60
 QY 61 GLAWIFPHIRNKTSFIFYLKXIVVADIMLTLPFRIVHDAGFGPWYFKPILCRYSTVL 120
 DB 61 GLAWIFPHIRNKTSFIFYLKXIVVADIMLTLPFRIVHDAGFGPWYFKPILCRYSTVL 120
 QY 121 FANNYTSIVFGLISIDRYLKVYKVPEDSRNYSTTFPKVYSGVCWVMVNLSPNIIIT 180
 DB 121 FANNYTSIVFGLISIDRYLKVYKVPEDSRNYSTTFPKVYSGVCWVMVNLSPNIIIT 180
 QY 181 NGOPTEDNIDHDSKLSKSPFGVGMHTAVYVNSCLPVAVLVILIGCYAISRIYHKSROF 240
 DB 181 NGOPTEDNIDHDSKLSKSPFGVGMHTAVYVNSCLPVAVLVILIGCYAISRIYHKSROF 240
 QY 241 ISQSRKRKHNSIRVVAVVFTCELPYHLGRIPFTFSHDLRLDESAQKILYYCKEITL 300
 DB 241 ISQSRKRKHNSIRVVAVVFTCELPYHLGRIPFTFSHDLRLDESAQKILYYCKEITL 300
 QY 301 FLSACNVCLDPIITFPMCRSFSRPLFKSNIRTSSEIRISQVRSRVRITYDYTDV 358
 DB 301 FLSACNVCLDPIITFPMCRSFSRPLFKSNIRTSSEIRISQVRSRVRITYDYTDV 358
 QY 301 FLSACNVCLDPIITFPMCRSFSRPLFKSNIRTSSEIRISQVRSRVRITYDYTDV 358
 DB 301 FLSACNVCLDPIITFPMCRSFSRPLFKSNIRTSSEIRISQVRSRVRITYDYTDV 358
 RESULT 2
 ID GP87_MOUSE STANDARD; PRT; 358 AA.
 AC 099WT7, Q864Y7; -;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable G protein-coupled receptor GP87.
 GN GP87.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 RN NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21172992; PubMed=11273702;
 RT Wittenberger T., Schaller H.C., Hellebrand S.,
 RT "An expressed sequence tag (EST) data mining strategy succeeding in
 RT the discovery of new G-protein coupled receptors.";
 RL J. Mol. Biol. 307:799-813(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=22354683; PubMed=12466851;
 RA Okazaki Y., Furuno M., Kaenaka T., Adachi J., Bono H., Kondo S.,
 RA Nikiado I., Oseco N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojohori T.,
 RA Baldarelli R., Hill D.P., Bulc C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dirigant T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Giesi C., Godzik A., Gough J.,
 RA Grimmond S., Guentrich S., Hirokawa N., Jackson J.J., Jarvis E.D.,
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konegaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maitais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numa K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
 RA Sultana R., Takemura Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wynshaw-Boris A., Yamagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yaenishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,

RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs";
 RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF295366; AAK01866.1; -;
 DR EMBL; AK080394; BAC37905.1; -;
 DR MGI; MGI:1934133; Gpr87.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008109; P2Y13_Purinocptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSN.
 DR PRINTS; PR01735; P2Y13_P2Y13PRNCPTR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; transmembrane; glycoprotein.
 FT DOMAIN 1 47
 FT TRANSMEM 48 68
 FT DOMAIN 69 75
 FT TRANSMEM 76 96
 FT DOMAIN 97 116
 FT TRANSMEM 117 137
 FT DOMAIN 138 159
 FT TRANSMEM 160 180
 FT DOMAIN 181 208
 FT TRANSMEM 209 229
 FT DOMAIN 230 256
 FT TRANSMEM 257 277
 FT DOMAIN 278 297
 FT TRANSMEM 298 318
 FT DOMAIN 319 358
 FT DISULFID 114 192
 FT CARBOHYD 4 4
 FT CARBOHYD 24 24
 FT CARBOHYD 33 33
 FT CONFLICT 1 1
 FT CONFLICT 11 11
 SQ SEQUENCE 358 AA; 41413 MW; 6D258B98CB3BE4B9 CRC64;
 Query Match 92.4%; Score 1731; DB 1; Length 358;
 Best Local Similarity 91.3%; Pred. No. 1.7e-106;
 Matches 327; Conservative 17; Mismatches 14; Indels 0; Gaps 0;

QY 1 MGFNLTTLAKLPNNELHGOESHNSGNRSDPGKNTLHNEFDITVLPVLTITFVASILLN 60
 DB 1 MGLNLTTLTKLPNNELHGOESHNSGNRSDPGKNTLHNEFDITVLPVLTITFVASILLN 60
 QY 61 GLAVNIPFHIRNKTSFIYFKNIIVADLIMLTTPFPRIVHDAFGFWPKFLICRYTVL 120
 DB 61 GLAVNIPFHIRNKTSFIYFKNIIVADLIMLTTPFPRIVHDAFGFWPKFLICRYTVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLVNRPFGSGSMYSTFTFTVLSVCWVMVMAVLSNIIIT 180
 DB 121 FYANNYTSIVFLGLISIDRYLVNRPFGSGSMYSTFTFTVLSVCWVMVMAVLSNIIIT 180
 QY 181 NGOPTEDNIDHDSKLSPLGVKMTAVTVYNSCLFPAVALVILIGCIATISRIYHSSRF 240
 DB 181 NGOPTEDNIDHDSKLSPLGVKMTAVTVYNSCLFPAVALVILIGCIATISRIYHSSRF 240
 QY 241 ISQSSRRKRGNSIRVVAVVFTCPFLPHLCRIPTFFSHLDRLDLSAOKIIYYCKEITL 300
 DB 241 ISQSSRRKRGNSIRVVAVVFTCPFLPHLCRIPTFFSHLDRLDLSAOKIIYYCKEITL 300

QY 301 FLASACVCLDPIIYFMCRSFRRLLFKSNIRTSSESIRLSQYRRSEVRRIYDYTDV 358
 DB 301 FLASACVCLDPIIYFMCRSFRRLLFKSNIRTSSESIRLSQYRRSEVRRIYDYTDV 358
 RESULT 3
 ID P2YX_HUMAN STANDARD; PRT; 338 AA.
 AC Q15391;
 DT 15-01-1998 (Rel. 36, Created)
 DT 15-01-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE UDP-glucose receptor (G protein-coupled receptor GPR105).
 GN GPR105 OR KIAA0001.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP TISSUE=Bone marrow;
 RC MEDLINE=96051387; PubMed=7584026;
 RX Nomura N., Miyajima N., Sazuka T., Tanaka A., Kawarabayashi Y.,
 RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;
 RT "Prediction of the coding sequences of unidentified human genes. I.
 RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by
 RT analysis of randomly sampled cDNA clones from human immature myeloid
 RT cell line KG-1.";
 RL DNA Res. 1:27-35(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21426338; PubMed=11524702;
 RA Joensuu T., Haemelaenen R., Yuan B., Johnson C., Tegelerberg S.,
 RA Gaepartini P., Zelante L., Pivola U., Pekariinen L., Lehesjoki A.-E.,
 RT "Mutations in a novel gene with transmembrane domains underlie Usher
 RT syndrome type 3.";
 RL Am. J. Hum. Genet. 69:673-684(2001).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=20219108; PubMed=10753868;
 RA Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Freeman K.,
 RA Foley J.J., Zhu Y., McLaughlin M.M., Murdoch P., McMillan L.,
 RA Trill J., Swift A., Aiyar N., Taylor P., Vawter L., Mehed S.,
 RA Szekeres P., Herliu G., Scott C., Watson J.M., Murphy A.J., Duzic E.,
 RA Klein C., Bergsma D.J., Wilson S., Livi G.P.;
 RT "A G protein-coupled receptor for UDP-glucose.";
 RL J. Biol. Chem. 275:10767-10771(2000).
 CC -1- FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled to
 CC G-proteins. Not activated by ATP, ADP, UTP or AMP.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Highest expression in the placenta, adipose
 CC tissue, stomach and intestine, intermediate levels in the brain,
 CC spleen, lung and heart, lowest levels in the kidney.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; D13626; BA02791.1; -;
 DR EMBL; AF456925; AAL47764.1; -;
 DR Genbank; HGNC:16442; GPR105.
 DR GO; GO:0016021; C:intracellular to membrane; NAS.
 DR GO; GO:0045029; F:UDP-activated nucleotide receptor activity; NAS.
 DR GO; GO:0007186; F:G-protein-coupled receptor protein signalin. . .; NAS.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR005466; UDPG_receptor.
 DR Pfam; PF00001; 7tm_1; 1.

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DR PRINTS; PRO0237; GPCRHDOPSN.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29
FT TRANSMEM 30 50
FT DOMAIN 51 55
FT TRANSMEM 56 76
FT DOMAIN 77 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 188
FT TRANSMEM 189 209
FT DOMAIN 210 234
FT TRANSMEM 235 255
FT DOMAIN 256 278
FT TRANSMEM 279 299
FT DOMAIN 300 338
FT DISULFID 94 172
FT CARBOHYD 3 3
FT CARBOHYD 161 161
SQ SEQUENCE 338 AA; 38971 MW; 8DBE7C782CB4753D CRC64;

Query Match
Best Local Similarity 41.0%; Score 768.5; DB 1; Length 338;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

QY 44 VLPVLTILFVASILINGIAWIFPHIRKNTSPFLYKNIVADLIMLTPTPRIVHDAG 103
DB 24 IIPVLCVWFVIGILINGVSGWIFVPSKSGFIYLNKIVADLIMLTPTPRIVHDAG 83
QY 104 FGPWFYKFLCYSTVLFYANNVTSIVELGLSIDRYLVKVPFGDSRWYSTTFKULSV 163
DB 84 LBPWOLNPFVCKVASLFTVNNVTSIVELFGLISPDYVIVPVLMTSPFQSVSEKLSLV 143
QY 164 CVMVIMAVLSPENIILITNGOPTEDNIDHDSKLSPLGVMTAVTVYVNSCLFVAVLVILI 223
DB 144 IYMMMLLAVNIIITLNGSVAEVQIKIEKLSLGRMHKASNYIPAFIMWIFLLI 203
QY 224 GCYVIAISRYTHKS-RQTSQSRKRNQSRVAVVFTFPLPYHLCRIPFTSHDR 282
DB 204 VYTTATIKKIFKSHKSNSTSVKKSRRNFISVTFVFCVFEVYHIAIRIYTSQGEA 263
QY 283 LIDESAOKIYCKEITLFLSACNVCIDPIITFPMCRSSRLFKSNRTSESIRSLQ 342
DB 264 HVSQSKELRYMKETLILSLANVCIDPIITFPLCQPREITLCKLHLPLKQNDLDS 323
QY 343 SVRSEVR 351
DB 324 RIKRGNTTL 332

RESULT 4
P2YX MOUSE STANDARD; PRT; 338 AA.
AC 09S6G;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE UDP-glucose receptor (G protein-coupled receptor GPR105).
GN GPR105.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN NCB1_TaxID=10090;
RA Lee B.C., Scadden D.T.;
RP "7 transmembrane G protein coupled receptor from hematopoietic
RT progenitors."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.

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RN N
RP SEQUENCE FROM N.A.
RC TISSUE-Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marnett K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Rosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Guarnatone P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hylk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for UDP-glucose coupled to G-proteins (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC
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CC
DR EMBL; AF177211; AACG9275.1; -.
DR EMBL; BC058558; AAH58558.1; -.
DR MGD; MGI:2155705; Gpr105.
DR GO; GO:0016021; C: integral to membrane, ISS.
DR GO; GO:0045029; F: UDP-activated nucleotide receptor activity, ISS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signaln. .; ISS.
DR InterPro; IPR000276; GPCR Rhodpsn.
DR InterPro; IPR005466; UDP_g_receptor.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PRO0237; GPCRHDOPSN.
DR PRINTS; PRO1655; UDPGLUCOSER.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29
FT TRANSMEM 30 50
FT DOMAIN 51 55
FT TRANSMEM 56 76
FT DOMAIN 77 96
FT TRANSMEM 97 117
FT DOMAIN 118 139
FT TRANSMEM 140 160
FT DOMAIN 161 188
FT TRANSMEM 189 209
FT DOMAIN 210 234
FT TRANSMEM 235 255
FT DOMAIN 256 278
FT TRANSMEM 279 299
FT DOMAIN 300 338
FT DISULFID 94 172
FT CARBOHYD 3 3
FT CARBOHYD 161 161
SQ SEQUENCE 338 AA; 38861 MW; 437650622A684E CRC64;

Query Match
Best Local Similarity 39.6%; Score 742.5; DB 1; Length 338;
Matches 147; Conservative 64; Mismatches 97; Indels 1; Gaps 1;

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Matches 149; Conservative 67; Mismatches 116; Indels 7; Gaps 3;

QY 22 NSGRSDGKNTLHNEFDIVLPVLYLIFVASILNGLAVWFFHIRKTSIFPYL 81
 DB 2 NNSITTDPNPCSNNTLITKOIIPVLGYWFIITGLLNGISGMFFVPSKSIITLK 61
 OY 82 NIVVADLIMTLTPPRIVHDAGFGPMYFKILCRYSVLFPYANNYSIVFLGLISIDRYL 141
 DB 62 NIVVADLIMTLTPPRIVHDAGFGPMYFKILCRYSVLFPYANNYSIVFLGLISIDRYL 121
 OY 142 KVVXKPGDSRMYSITFTKVLVSCVWVIMAVLSLPIIITNGQPEDNIDHCSKLSPLGV 201
 DB 122 KIVKPLTSLIVQSVNYSKLSLTVLWMLMLLAVPNIITLNGQVKEVTKIQCEMLNEHGR 181
 OY 202 KMTAVTVVNSCLFPAVLVILIGCIYASRYIHKS---SRQFISGSSRRKRNQSIIRVV 258
 DB 182 KMHKSNYIFVSIFFVWVFLILVFTYATITRKIFKSHLSRK--NSTSVKRSNRIFSI 239
 OY 259 AVFPTCLPYHLCRIPFTFSHLDRLLDSAQKILYYCKEITLFLSACVNCCLDPIIYFPMC 318
 DB 240 LVFVVCVFPYHARIPYTKSQTEGHSQRTKETLIXAEFTLLLSAANVCDDPIIYFPLC 299
 OY 319 RSPFRRLPKKSNITRSESIRSLQSVRSSEVRIYYDITD 357
 DB 300 QPFRVLNKLKMLMSLVKQNDLEVSRTKRENA--IHSTID 336

RESULT 5
 P2YC_RAT STANDARD; PRT; 343 AA.
 AC Q9CEPK4;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley;
 RX MEDLINE=21037966; PubMed=1196645;
 RA Hollopeter G., Jentzen H.-M., Vincent D., Li G., England L., Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J., Conley P.B.;
 RA "Identification of the platelet ADP receptor targeted by antithrombotic drugs";
 RT Nature 409:202-207(2001).
 RL Nature 409:202-207(2001).
 CC -1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that inhibit the adenylyl cyclase second messenger system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC EMBL; AF134450; AAC48945.1; -
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR InterPro; IPR005394; P2Y12_purinocptor.
 DR Pfam; PF00001; Tcm_1; 1
 DR PRINTS; PR00237; GPCR_Rhodopsin.
 DR PRINTS; PR01569; P2Y12_P2Y12.
 DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.

FT DOMAIN 1 31
 FT TRANSSEM 32 52
 FT DOMAIN 53 64
 FT TRANSSEM 65 85
 FT TRANSSEM 86 105
 FT TRANSSEM 106 126
 FT TRANSSEM 127 148
 FT TRANSSEM 149 169
 FT TRANSSEM 170 197
 FT TRANSSEM 198 218
 FT TRANSSEM 219 239
 FT TRANSSEM 240 260
 FT TRANSSEM 261 287
 FT TRANSSEM 288 308
 FT TRANSSEM 309 343
 FT DISULFD 103 181
 FT CARBOHYD 7 7
 FT CARBOHYD 12 12
 SQ SEQUENCE 343 AA; 39047 MW; 7AE0AFCE6674136 CRC64;

Query Match 37.4%; Score 700.5; DB 1; Length 343;
 Best Local Similarity 43.8%; Pred. No. 3.4e-39;
 Matches 134; Conservative 66; Mismatches 103; Indels 3; Gaps 2;

QY 23 NSGRSDGKNTLHNEFDIVLPVLYLIFVASILNGLAVWFFHIRKTSIFPYL 80
 DB 10 SANTSIIPGISTLSRDKIQVLPPLLYTLVFPAGLITNGLAWRIFQHSKSFIFL 69
 OY 81 NIVVADLIMTLTPPRIVHDAGFGPMYFKILCRYSVLFPYANNYSIVFLGLISIDRY 140
 DB 70 KNTVSLDMLITLTPPRKILSDAKLGHILRTLVQCVTSVTFYFMYISISFLGITIDRY 129
 OY 141 LKVVKPGDSRMYSITFTKVLVSCVWVIMAVLSLPIIITNGQPEDNIDHCSKLSPLG 200
 DB 130 LKTRPFTSSPSMLGAKILSVAIMFPLSLPNMLTRRPDKDITKCSFLKSEBG 189
 OY 201 VKMTAVTVVNSCLFPAVLVILIGCIYASRYIHKS--SRQFISGSSRRKRNQSIIRVV 259
 DB 190 LVMEIIVNYIQVIFWINEFLIVICYSLTIELVRSYRTGSAKAPKRVNINIKFIIA 249
 OY 260 VFTCTCLPYHLCRIPFTFSHLDRLLDSAQKILYYCKEITLFLSACVNCCLDPIIYFPMC 319
 DB 250 VFICFVFPYHARIPYTKSQTEGHSQRTKETLIXAEFTLLLSAANVCDDPIIYFPLC 309
 OY 320 SFSRRL 325
 DB 310 SFRNSL 315

RESULT 6
 P2YC_MOUSE STANDARD; PRT; 347 AA.
 AC Q9CEPV9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12).
 GN Mus musculus (Mouse).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NC NCB1_TaxID=10090;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Komio H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamaneke I., Saito T., Okazaki Y., Gojodori T., Bono H., Kaubawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schirml L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Maehio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldirelli P., Barsch G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinch S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Maehima M., Mazzarelli J., Mombarts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Sorch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilmberg L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohseki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
[12]
RP SEQUENCE FROM N.A.
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Urdahl H., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marz M.A.,
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-1- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
inhibit the adenylyl cyclase second messenger system (By
similarity).
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC or send an email to license@isb-sib.ch).

CC EMBL AK013804; BAB29000.1; -
CC EMBL AK014807; BAB29561.1; -
CC EMBL BC025428; AAH25428.1; -
CC EMBL BC027381; AAH27381.1; -
CC MGD; MGI:1918089; P2ry12.
DR GO:GO:0005887; C:integral to plasma membrane; IC.
DR GO:GO:0001609; F:adenosine receptor activity; G-protein coupled; IMP.
DR GO:GO:0001621; F:platelet ADP receptor activity; IMP.
DR GO:GO:0007188; P:G-protein signaling; coupled to cAMP nucleo. . .; IMP.
DR GO:GO:0030168; P:platelet activation; IMP.
DR InterPro; IPR002026; GPCR_Rhodopsin.
DR InterPro; IPR005394; P2ry12_purinoceptor.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsin.
DR PRINTS; PR01569; P2ry12_P2ry12.
DR PROSITE; PS00237; G_PROTEIN_RECP_F1_1; FALSE NEG.
DR PROSITE; PS00262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; transmembrane; glycoprotein.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 64
FT TRANSMEM 65 85
FT DOMAIN 86 105
FT DOMAIN
EXTRACELLULAR (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 106 126
FT DOMAIN 127 148
FT TRANSMEM 149 169
FT TRANSMEM 170 197
FT TRANSMEM 198 219
FT TRANSMEM 219 239
FT TRANSMEM 240 260
FT TRANSMEM 261 287
FT TRANSMEM 288 308
FT TRANSMEM 309 347
FT DISULFID 103 181
FT CARBOHYD 7 7
FT CARBOHYD 12 12
FT CONFLICT 3 3
SQ SEQUENCE 347 AA; 39473 MW; F1074885E7B025F1 CMC64;
Query Match 37.1%; Score 696; DB 1; Length 347;
Best Local Similarity 43.3%; Pred. No. 6.7e-39;
Matches 136; Conservative 61; Mismatches 101; Indels 16; Gaps 2;
QY 28 DQFGNTTLN-----EFDITVPLVLIIFVASTLNGLAVMIFPHRN 72
DB 2 DVGAVNTTSANTTSPGTSGLCVADYKLTQVLPFLVTLVFPAGLITSLMRIFFOIRS 61
QY 73 KTSFFLYKNIVADLMTLTPPRIVADAGFGWYFELICRYTSVLFYANMTTSIVFL 132
DB 62 KSNFIFLKNIVISDLMLTLPFKILSDALGAGPRLTVCQTSVTFYMTISISFL 121
DB 133 GLISIDRYLKVKGPGSRMYSITFTKYLSCVAVINAVLSLPIILITNGOPTEDNIHDC 192
QY 122 GLITIDRYLKTTRPKTSSPENLGAKLISVIAVAFELLSLPMIILNRRPKDKVTKC 181
DB 123 SKLSPGVKMHVATVYNSCLFVAIVILIGCIATISRYHRS-SRQFISQSRKXKH 251
QY 193 SFLSEFSLVHWEIVNYICQVTFINPLIVVCSLTTELKRYRYTRGSAKPKKKVN 241
DB 182 QSRVAVAFPTCELPYHLCRIPTFSDHDLDESAOKILVYCKEITLPLACNVCLDP 311
QY 242 VKVPIIIVFICVPHFPAIPIYTLSTQTRAVFPCSAENTLFYKKESTWLTSLNACIDP 301
DB 312 IYFPMCRSPSRRL 325
QY 302 FIVEFLCKSPFNSL 315
DB
RESULT 7
P2YC_HUMAN STANDARD; PRT; 342 AA.
AC Q9H244;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y (ADP))
DE (ADP-glucose receptor) (ADPG-R) (P2Y (AC)) (P2Y (cyc)) (P2Y (AC))
DE (SP1999).
GN P2RY12 OR HOKR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21037966; PubMed=11196645;
RA Hollopeter G., Jantzen H.-M., Vincent D., Li G., Englund L.,
RA Ramakrishnan V., Yang R.-B., Nudsen P., Nudsen A., Julius D.J.,
RA Conley P.B.,
RT "Identification of the platelet ADP receptor targeted by
antithrombotic drugs.";
RL Nature 409:202-207(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Hypothalamus;
RX MEDLINE=21269433; PubMed=11104774;
FT

Db 304 SFRNSLI--SMKCPNATSLSQDNKKE 330

RESULT 8

ID GPR86 HUMAN STANDARD; PRT; 333 AA.

AC GPR86; O81UT5; Q8TUD7;

DT 10-OCT-2003 (Rel. 42, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DE Probable G protein-coupled receptor GPR86 (P2Y purinoceptor 13) (P2Y13).

GN GPR86 OR GPR94 OR FKSG77.

OS Homo sapiens (human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Amalgala, Caudate, Fetal brain, and Placenta;

RX MEDLINE=21172992; PubMed=11273702;

RT Wittenberger T., Schaller H.C., Heilebrand S.;

RT "An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors.";

RL J. Mol. Biol. 307:799-813 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21458557; PubMed=11574155;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arhitek O., Lewis T., Evans J.F., George S.R., O'Powd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor genes.";

RL Gene 275:83-91 (2001).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=21538899; PubMed=11546776;

RA Communi D., Gonzalez N.S., Dethieux M., Brezillon S., Lannoy V., Parmentier M., Boeynaems J.-M.;

RT "Identification of a novel human ADP receptor coupled to Gi.";

RL J. Biol. Chem. 276:41479-41485 (2001).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE=22040266; PubMed=12044878;

RA Takada S., Kadowaki S., Haga T., Takesu H., Mitaku S.;

RT "Identification of G protein-coupled receptor genes from the human genome sequence.";

RL FEBS Lett. 520:97-101 (2002).

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Heart;

RX Wang Y.-G., Gong L.;

RT "Molecular cloning of FKSG77, a novel gene encoding a putative G-protein-coupled receptor.";

RL Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.

RN [6]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Straube R.L., Pelngold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Boeck S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hultik S.W., Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Scherich A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

CC -1- FUNCTION: Orphan receptor. Seems to be a G(i)-coupled receptor displaying a high affinity for ADP. Might play a role in hematopoiesis and the immune system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- TISSUE SPECIFICITY: Strong expression in spleen and adult brain. Lower expression in placenta, lung, liver, spinal cord, thymus, small intestine, uterus, stomach, testis, fetal brain, and adrenal gland. Not detected in pancreas, heart, kidney, skeletal muscle, ovary or fetal aorta. Clearly detected in lymph node and bone marrow, weakly detected in peripheral blood mononuclear cells (PBMC) and in peripheral blood leukocytes (PBL), but not detected in polymorphonuclear cells (PMN). In the brain, detected in all brain regions examined.

CC -1- MISCELLANEOUS: Stimulation by ADP in stably transfected CHO cells resulted in inhibition of adenylyl cyclase and the phosphorylation of the MAP kinases MAPK3 and MAPK1 in a pertussis toxin-sensitive way. Inhibition of adenylyl cyclase and phosphorylation of the MAP kinases are transduction mechanisms that involve G(i) proteins.

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

CC -----

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CC -----

CC EMBL; AF295368; AAK01864.1; -

CC EMBL; AF411113; AAL26484.1; -

CC EMBL; AF406692; AAL01038.1; -

CC EMBL; AB083597; BAB89310.1; -

CC EMBL; AF345565; AAK29068.1; -

CC EMBL; BC041116; AAA41116.2; -

CC GeneW; HGNC:4537; GPR86.

CC MIM; 606380; -

CC DR GO; GO:0016021; C:Integral to membrane, NAS.

CC DR GO; GO:0016526; F:G-protein coupled receptor activity, unknow. . .; NAS.

CC DR InterPro; IPR000276; GPCR Rhodpsn.

CC DR InterPro; IPR008109; P2Y13_purinocptor.

CC DR Pfam; PF00001; 7tm_1; 1.

CC DR PRINTS; PR00237; GPCRHRDOPSN.

CC DR PRINTS; PR01735; P2Y13PRNCPTR.

CC DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.

CC DR PROSITE; PS50262; G-PROTEIN RECP_F1_2; 1.

CC KW G-protein coupled receptor; Transmembrane; Glycoprotein. EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 1 28

CC FT TRANSMEM 29 49

CC FT DOMAIN 50 56

CC FT TRANSMEM 57 77

CC FT DOMAIN 78 96

CC FT TRANSMEM 97 117

CC FT DOMAIN 118 140

CC FT TRANSMEM 141 161

CC FT DOMAIN 162 190

CC FT TRANSMEM 191 211

CC FT DOMAIN 212 231

CC FT TRANSMEM 232 252

CC FT DOMAIN 253 279

CC FT TRANSMEM 280 300

CC FT DOMAIN 301 333

CC FT DISULFID 95 173

CC FT CARBOHYD 2 2

CC FT CARBOHYD 10 10

CC FT CARBOHYD 264 264

CC FT CONFLICT 158 158

CC FT SEQUENCE 333 AA; 38440 MW; F234ABBS0016DF34 CRC64;

Query Match 37.0%; Score 692.5; DB 1; Length 333;
 Best Local Similarity 41.1%; Pred. No. 11e-38;
 Matches 127; Conservative 67; Mismatches 96; Indels 19; Gaps 4;

Query 33 NTTLNNE-----DT-----IVPLVYLIFVASILNGLAWIPFHIRKTSFIFVL 80
 2 NTVWOGNRSRBCRDRIYQVLPALYTVFVLGIILNTLALVAFHIBESSFIYIL 61
 Db 81 KNIVADILMTLTPFRIVHDAGFGPWYFKFLCRYTVLFPYANNYSIVFLGISIDRY 140
 62 KNTLVADILMTLTPFRIVHDAGFGPWYFKFLCRYTVLFPYANNYSIVFLGISIDRY 121
 Qy 141 LKVVKPEPDSRMYSITFTKVLVSVGVVIMAVLSLNTILNQPFEDINHDSKSLPLG 200
 122 LKTRPLNIPFKPEFVFAKTVSIFLWFLPFLSLPMTLSNKEATPSSVKKASLKGFLV 181
 Db 201 VKMHTAVTVYNSCLFVAVLVILIGCYAISRYIHKSROFISQSRKKNQISIR----V 256
 182 LKMGMVNNICOFITWTVFILMLVYVIAKKVDSYK---SKKDKRNNKXLEGKVFV 238
 Qy 257 VVAVFCTFLPYHLCRIPFTSHDLRLDESQKILYCKEITFLSACNVCLDPIIYF 316
 239 VVAVFVCFAPFHFARVYTHSQTNNKTDCLQNLFLAKETTLFLAATNICMDPLIYIF 298
 Db 317 MCRSFSRL 325
 299 LCKKTEKL 307

RESULT 9
 P2YC_MACFA STANDARD; PRT; 342 AA.
 ID P2YC_MACFA Q95K3; Q9BG78;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P2Y purinoceptor 12 (P2Y12).
 GN P2Y12.
 OS Macaca fascicularis (Craab eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheidae; Macaca.
 NC NCB1_Taxid=9541;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE:Frontal cortex, and Medulla oblongata;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 CC -1 FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
 CC inhibit the adenylyl cyclase second messenger system (By
 CC similarity).
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1 SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB056385; BAB33041.1; -;
 DR EMBL: AB063981; BAB60747.1; -;
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR InterPro: IPR005394; P2Y12_purinocptor.
 DR InterPro: IPR008109; P2Y12_purinocptor.
 DR Pfam: PF00001; 7cm1.1.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.

PRINTS: PR01569; P2Y12PNCPTP.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KM TRANSMEM 1 25
 FT DOMAIN 26 46
 FT TRANSMEM 47 58
 FT DOMAIN 59 79
 FT TRANSMEM 80 99
 FT DOMAIN 100 120
 FT TRANSMEM 121 142
 FT TRANSMEM 143 163
 FT TRANSMEM 164 191
 FT TRANSMEM 192 212
 FT TRANSMEM 213 233
 FT TRANSMEM 234 254
 FT TRANSMEM 255 281
 FT TRANSMEM 282 302
 FT TRANSMEM 303 342
 FT DISULFD 97 175
 FT CARBOHYD 6 6
 FT CARBOHYD 13 13
 FT CONFLICT 49 49
 FT CONFLICT 89 89
 SQ SEQUENCE 342 AA; 39479 MW; E93FC6BBPFSFC4C CXC64;

Query Match 36.6%; Score 686.5; DB 1; Length 342;
 Best Local Similarity 41.6%; Pred. No. 2.8e-38;
 Matches 137; Conservative 69; Mismatches 114; Indels 9; Gaps 5;

Query 25 NRSDEGKNTL---HNEFDIVPVLYLIFVASILNGLAWIPFHIRKTSFIFVL 81
 6 NLTSAPG-NTSLCTRDYKITQVLPFLVTVFVGLINSLAMRFQIRKSNFIPLK 64
 Db 82 NIIVADILMTLTPFRIVHDAGFGPWYFKFLCRYTVLFPYANNYSIVFLGISIDRYL 141
 65 NTVISDLMLITLTPFRIVHDAGFGPWYFKFLCRYTVLFPYANNYSIVFLGISIDRYL 124
 Qy 142 KVVKPEPDSRMYSITFTKVLVSVGVVIMAVLSLNTILNQPFEDINHDSKSLPLGV 201
 125 KTRPFPKTSNKNKILGAKILSVLWAFWFLPFLSLPMTLSNKEATPSSVKKASLKGFLV 184
 Db 125 KTRPFPKTSNKNKILGAKILSVLWAFWFLPFLSLPMTLSNKEATPSSVKKASLKGFLV 184
 Qy 202 KMHHTAVTVYNSCLFVAVLVILIGCYAISRYIHKS--SRQFISQSRKKNQISIRVVA 259
 185 VMHEIVNITCOVIFINFLVIVCTLTLEKLSRYVTRGVKPKR-KNVVAKFIITA 243
 Qy 260 VFTCTFLPYHLCRIPFTSHDLRLDESQKILYCKEITFLSACNVCLDPIIYFMC 319
 244 VFTCTFLPYHLCRIPFTSHDLRLDESQKILYCKEITFLSACNVCLDPIIYFMC 303
 Db 320 SFSRRLFKKSNIRKTSIRSLQSVRSE 348
 304 SFRSLI--SMLKCPNSATSQSDRRKKE 330

RESULT 10
 P2YX_RAT STANDARD; PRT; 305 AA.
 ID P2YX_RAT O35881;
 AC 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE UDP-glucose receptor (G protein-coupled receptor GPR105) (VTR 15-20).
 GN GPR105.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_Taxid=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97439647; PubMed=9295203;
 RA Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Duman R.S.;

CC -1- FUNCTION: Orphan receptor. Seems to be a G(i)-coupled receptor
 CC displaying a high affinity for ADP. Might play a role in
 CC hematopoiesis and the immune system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AK008013; BAB25409.1; -
 DR EMBL; AK0083264; BAC38835.1; -
 DR EMBL; AK038560; BAC30043.1; -
 DR MGD; MGI:1921441; Gpr86.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008109; P2Y13_purinocptor.
 DR InterPro; IPR005466; UDPG_receptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR01735; P2Y13_Purinocptor.
 DR PRINTS; PR01655; UDPGLUCOSER.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein.
 KW DOMAIN 1 31
 FT TRANSMEM 32 52
 FT DOMAIN 53 60
 FT TRANSMEM 61 81
 FT DOMAIN 82 101
 FT TRANSMEM 102 122
 FT DOMAIN 123 144
 FT TRANSMEM 145 165
 FT DOMAIN 166 193
 FT TRANSMEM 194 214
 FT DOMAIN 215 237
 FT TRANSMEM 238 258
 FT DOMAIN 259 281
 FT TRANSMEM 282 302
 FT DOMAIN 303 337
 FT DISULFID 99 176
 FT CARBOHYD 6 6
 FT CARBOHYD 14 14
 FT CARBOHYD 266 266
 FT CONFLICT 197 197
 FT CONFLICT 237 237
 SQ SEQUENCE 337 AA; 38727 MW; 2C1A7B969D5CED48 CRC64;
 Query Match 35.5%; Score 666; DB 1; Length 337;
 Best Local Similarity 38.4%; Pred. No. 5.9e-37;
 Matches 127; Conservative 72; Mismatches 120; Indels 12; Gaps 3;
 Oy 17 GOESHNSNRDDEGKNTTLNNEPTVLPVLYLIIFASILLGLAWIFPHIRKTSF 76
 Db 9 GMOGFNKSERCPDRMTOL-----LFPVLYTVFVLAGILLNVALMVPHIPSNSTF 61
 Oy 77 IFYKNIIVADLIMLTLPRIYHDAGRPVYFKILCRYSVLYFYAMVTSIYFLGIS 136
 Db 62 IYVLYKNTLVADLIMLMPKILSDSHLAPWOLRFVTLSSVYFETMYGIMMLGLIA 121
 Oy 137 IDRYLYKVPFGDSRMYSITFTKVLSCVWVIMAVLSPNLIITNGOPTEDNIHDSRLK 196
 Db 122 FDRFLKIMPRKFTVFKTAFAKTVSISVMSLMPFISLPNML-NKEATPSVKKCAELK 180
 Oy 197 SPLGVKHTATVYNSCLFVAVLVILICGTALISYTHKSRQFSSOSRKRKNQSRIV 256
 Db 181 SPLGLMHWQVSHTCQFLFMAVFIIMLLFYAVITTKVYNSYRKFKFSKDSRKRLEVKFI 240
 Oy 257 VVAVFETFLPYHLCRIPTFSHLDRLDDESAOKILYCKETLFLSACNVCLDPIIYVF 316

Db 241 VMAVFVFCAPLHFVRIPYVTSQTTNKDCRLNQLFIKAEATLFLATTNICMPLIYII 300
 Oy 317 MCRSFSRRL-----FKSNIRRSISISLOS 343
 Db 301 LCKKFTQKVPVCRWKGARTAGSSSDHSSQT 331
 RESULT 12
 GP86_MACFA STANDARD; PRT; 245 AA.
 ID GP86_MACFA
 AC Q9BE53;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Probable G protein-coupled receptor GP86 (Fragment).
 GN GP86.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Frontal cortex;
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
 RA Suzuki Y., Sugano S., Hashimoto K.;
 RT "Isolation of full-length cDNA clones from macaque brain cDNA
 RT libraries.";
 RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor. Seems to be a G(i)-coupled receptor
 CC displaying a high affinity for ADP. Might play a role in
 CC hematopoiesis and the immune system (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AB056816; BAB9342.1; ALT_INIT.
 DR InterPro; IPR000276; GPCR_Rhodopsn.
 DR InterPro; IPR008109; P2Y13_purinocptor.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCR_Rhodopsn.
 DR PRINTS; PR01735; P2Y13_Purinocptor.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT NON TER 1 1
 FT DOMAIN <1 9
 FT TRANSMEM 10 30
 FT DOMAIN 31 35
 FT TRANSMEM 36 56
 FT DOMAIN 57 85
 FT TRANSMEM 86 106
 FT DOMAIN 107 126
 FT TRANSMEM 127 147
 FT DOMAIN 148 174
 FT TRANSMEM 175 195
 FT DOMAIN 196 245
 FT DISULFID 7 85
 SQ SEQUENCE 245 AA; 28371 MW; DDF91FF9332PA158 CRC64;
 Query Match 26.2%; Score 491.5; DB 1; Length 245;
 Best Local Similarity 40.6%; Pred. No. 1.1e-25;
 Matches 88; Conservative 50; Mismatches 72; Indels 7; Gaps 2;
 Oy 113 LCRTSYLVFYAMNTSIVFGLISIDRYLKVPFGDSRMYSITFTKVLSCVWVIMAVL 172

Db 6 VCRSLSVFVETMYGVILGLIADRFLKIIRPLANIPLKKTVAQTVSVFIMSEFFFI 65
 Qy 173 SLPLIILNGOPTEDNIHDCSKLSPGLGVKHTAVYVNSCLFVAVLILGCIYAIISRY 232
 Db 66 SLPLMILNKERTPSSVKKKASIKGPDGLKMHQIVNNISQIFWIVFVIMVFIYVIAKK 125
 Qy 233 IHKSSROPTISOSSRRKKRKNOSIR----VVAVVFPCFIPYHLCRIPEFESHDLRLDLSA 288
 Db 126 VYDSYRK--SKSKRRKNNKLEKGVFVAVVAFVCFAPFHTRYVYISQTNKTDCL 182
 Qy 289 QKILYCKEITLFLSACNVCLDPIIYFPMCSFSRRL 325
 Db 183 QNQLFIACKETLFLAATNINCMDPLIYIFLCKKFTKEL 219

RESULT 13
 ID_H963 HUMAN STANDARD; PRT: 319 AA.
 AC 014626;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable G protein-coupled receptor H963.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood monocytes;
 RX MEDLINE=98036061; PubMed=9370294;
 RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
 Golden-Fleet M., Kelleher K., Kriz R., Lavallie E.R., Metberg D.,
 Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
 RA "A genetic selection for isolating cDNAs encoding secreted proteins.";
 RL Gene 198:289-296(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21426338; PubMed=11524702;
 RA Joensuu T., Haemaelaenen R., Yuan B., Johnson C., Tegelberg S.,
 Gasparrini P., Zeilante L., Pirvola U., Pakarinen L., Lehesjoki A.-E.,
 RA de la Chapelle A., Sankila A.-M.;
 RA "Mutations in a novel gene with transmembrane domains underlie Usher
 syndrome type 3.";
 RL Am. J. Hum. Genet. 69:673-684(2001).
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
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 CC -----
 CC EMBL, AF002986; AAC51846.1; -;
 DR EMBL, AF411849; AAL47763.1; -;
 DR GO, GO:0016021; C:integral to membrane; NAS.
 DR GO, GO:0004930; G-G-protein coupled receptor activity; NAS.
 DR GO, GO:0007186; P-G-protein coupled receptor protein signalin. . .; NAS.
 DR InterPro, IPR000276; GPCR_Rhodopsn.
 DR Pfam, PF00001; 7tm_1.1.
 DR PRINTS, PR00237; GPCR_RHODOPSN.
 DR PROSITE, PS00337; G-PROTEIN RECP F1.1; 1.
 DR PROSITE, PS00262; G-PROTEIN RECP F1.2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 21
 FT TRANSMEM 22 42
 FT DOMAIN 43 48
 FT TRANSMEM 49 69
 FT 2 (POTENTIAL).
 FT 2 (POTENTIAL).

FT DOMAIN 70 89
 FT TRANSMEM 90 110
 FT DOMAIN 111 132
 FT TRANSMEM 133 153
 FT DOMAIN 154 181
 FT TRANSMEM 182 202
 FT DOMAIN 203 224
 FT TRANSMEM 225 245
 FT DOMAIN 246 268
 FT TRANSMEM 269 289
 FT DOMAIN 290 319
 FT CARBOHYD 3
 FT SEQUENCE 319 AA; 36754 MM; 79B9821C10841114 CRC64;
 SQ

Query Match 22.4%; Score 420.5; DB 1; Length 319;
 Best Local Similarity 29.6%; Pred. No. 6.1e-21;
 Matches 83; Conservative 64; Mismatches 126; Indels 7; Gaps 3;

Qy 49 YLIIFVASIILNGLAVMIFPHIR-NKTSFIYKNIIVADLIMLTPEPRIVHDAGGPW 107
 Db 21 FYLVFVGLIGSCRAIWAFLQKNNHRCVSIYLNILTLADRLTLALPVKIVDLGVAWP 80
 Qy 108 YKFLCRYSVLFYANNYTSIVFLGISIDRYLKVVPKFDSSNYSITFKVLSVCYW 167
 Db 81 KLKTFHCQVTFACLIYIMNYLSIIFLAFVSDIRCLQTHSKCIYRIQERGFAMSTVWL 140
 Qy 168 IMAVLSLPNIIILNGOPTEDNIHDCSKLSPGLGVKHTAVYVNSCLFV-AVLVILIGC 225
 Db 141 MWLLIMVPMNMTIPKIDIKESNVGCMERKKEFGNNMLNIFCVALFANSAIILISNC 200
 Qy 226 YIAISRYIHKSSROPTISOSSRRKKRKNOSIRVAVVAFVCFELPYHLCRIPEFESHDLRLD 285
 Db 201 LVINQLVRNNKNENY----PVMKKALINILVLTGYILCEVPYIVHPIYLSQTEVITD 256
 Qy 286 ESAQKILYCKEITLFLSACNVCLDPIIYFPMCSFSRRL 325
 Db 257 CSTRISLFAKEATVLLAVSNLCFDPILLYHLSKAFSSKV 296

RESULT 14
 ID_C172 MOUSE STANDARD; PRT: 309 AA.
 AC 0920A1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cysteinyll leukotriene receptor 2 (CysLTR2).
 GN CysLTR2 OR CysLTR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Heart;
 RX MEDLINE=21601669; PubMed=11591709;
 RA Hui Y., Yang G., Galiczenski H., Figueroa D.J., Austin C.P.,
 RA Copeland N.G., Gilbert D.J., Jenkins N.A., Funk C.D.;
 RA "The murine cysteinyl leukotriene 2 (CysLTR) receptor. cDNA and
 RT genomic cloning, alternative splicing, and in vitro
 RT characterization.";
 RL J. Biol. Chem. 276:47489-47495(2001).
 CC -1- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
 CC mediated via a G-protein that activates a phosphatidylinositol-
 CC calcium second messenger system. The rank order of affinities for
 CC the leukotrienes is LTC4 > LTD4 > LTE4.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Widely expressed at low levels, with highest
 CC expression in the spleen, thymus and adrenal gland, and lower in
 CC the kidney, brain and peripheral blood leukocytes.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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CC EMBL AF311658; AAK97354.1; -
 DR MGD; MGI:1917336; Cyt112.
 DR GO; GO:0016020; C:membrane; IDA.
 DR GO; GO:0001631; F:cysteineyl leukotriene receptor activity; IDA.
 DR InterPro; IPR004071; Cyaleuk receptor.
 DR InterPro; IPR002761; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR01533; CTSITRECPTR.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein.
 FT DOMAIN 1 26
 FT TRANSMEM 1 26
 FT DOMAIN 27 47
 FT TRANSMEM 48 56
 FT DOMAIN 57 77
 FT TRANSMEM 78 98
 FT DOMAIN 99 119
 FT TRANSMEM 120 138
 FT DOMAIN 139 159
 FT TRANSMEM 160 187
 FT DOMAIN 188 208
 FT TRANSMEM 209 229
 FT TRANSMEM 230 250
 FT DOMAIN 251 271
 FT TRANSMEM 272 292
 FT DOMAIN 293 309
 FT DISULFID 95 171
 FT CARBOHYD 14 14
 SQ SEQUENCE 309 AA; 35227 MW; 327B14A6BDDDA02 CRC64;

Query Match 20.1%; Score 376.5; DB 1; Length 309;
 Best Local Similarity 31.2%; Pred. No. 4,5e-18;
 Matches 101; Conservative 56; Mismatches 134; Indels 33; Gaps 12;

QY 23 SGNSSDGGKNTLNEFDIVLPVLYLIFVASILLGLAWIFPHI-IRNKTSPFIYFK 81
 DB 4 TGTBSSYNRNCTIEN-FKKEPFIYIYLIFFWGLNGFSYIVLQTCCKSTSVNVFLL 62
 QY 82 NIIVVADLIMTLTLPFRIVHAGFGPMYKFLICRYTSVLFYANMTYSIVFGLISIDRYL 141
 DB 63 NLATSDPLFISTLPPRADYIPRGSNWIFODLACRMWSISLVNMTYSIFLTVLSVARFQ 122
 QY 142 KVVKPGDGRMYSTFTK--VLSVCVWVIVAVLSLPHIILNQGPTEDNIHDC-----S 193
 DB 123 ATVHPF---RMHFVTSVRSAMWILGIIWVF--IMASSALLVNGEKNIIISCLSLSPQ 177
 QY 194 KLSKSLGKMTNAYVNVNSCLFVAVLVILIGCYIANSYIHKSSQFISQSRKKKHNS 253
 DB 178 KFKSL-LIMNHIAV---AVGFLPLTLTYCYLIILILAE--IPESGPRAHAKKA 229
 QY 254 IRVVV---AVFPTCLPYHLICRIPTFSHLDRLLDESOKIIVYKKEITLFLSACNVCLD 310
 DB 230 LTTIVIAMITPLCLCPYHALRT-----LHLVTWMDSCGDVIAKRVITLITMAAANSCFN 285
 QY 311 PIYFPCRSFGRRL--PKKSN 331
 DB 286 PFLYFAGENFKARLRAIFSKVL 309

RESULT 15
 PAFR_CAVPO STANDARD; PRT; 342 AA.
 ID PAFR_CAVPO
 AC P21556;
 DT 01-MAY-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).

GN PAFR.
 OS *Cavia porcellus* (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 CX NCBI_Taxid=10141;

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RX MEDLINE=91101726; PubMed=1846231;
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,
 RA Okada H., Toh H., Ito K., Miyamoto T., Shimizu T.;
 RT "Cloning by functional expression of platelet-activating factor
 RT receptor from guinea-pig lung.";
 RL Nature 349:342-346 (1991).

CC -1- FUNCTION: Receptor for platelet activating factor, a chemotactic
 CC phospholipid mediator that possesses potent inflammatory, smooth-
 CC muscle contractile and hypotensive activity. Seen to mediate its
 CC action via a G protein that activate a phosphatidylinositol-
 CC calcium second messenger system.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.

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CC EMBL X56736; CA440060.1; -
 DR PIR; S13638; S13638.
 DR InterPro; IPR002761; GPCR_Rhodopsn.
 DR Pfam; PF00001; 7tm1; 1.
 DR PRINTS; PR00237; GPCR_RHODOPSIN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.

FT DOMAIN 1 16
 FT TRANSMEM 17 38
 FT DOMAIN 39 54
 FT TRANSMEM 55 74
 FT DOMAIN 75 91
 FT TRANSMEM 92 113
 FT DOMAIN 114 133
 FT TRANSMEM 134 155
 FT DOMAIN 156 184
 FT TRANSMEM 185 205
 FT DOMAIN 206 233
 FT TRANSMEM 234 254
 FT DOMAIN 255 276
 FT TRANSMEM 277 296
 FT DOMAIN 297 342
 FT CARBOHYD 4 4
 FT CARBOHYD 169 169
 FT DISULFID 90 173
 SQ SEQUENCE 342 AA; 38984 MW; B6413B3A5C87B175 CRC64;

Query Match 20.0%; Score 375.5; DB 1; Length 342;
 Best Local Similarity 27.2%; Pred. No. 5.7e-18;
 Matches 96; Conservative 74; Mismatches 148; Indels 35; Gaps 9;

QY 22 NSGNRSDGPKNTLNEFDIVLPVLYLIFVASILLGLAWIFPHI---RNKTSPIY 78
 DB 4 NSSSRVD-----SEFRITLPIYISITIFVGLIINGVAVNWFALRYSKLNEIKI 54
 QY 79 YLKIIVVADLIMTLTLPFRIVHAGFGPMYKFLICRYTSVLFYANMTYSIVFGLISID 138
 DB 55 FMVNLTVADLILTLTLPMTIYVYSGNWIFPKFLCNLAGCLPINTYCSVAFLGVITYN 114

```

Oy 139 YLLKVKVPPGDSRMYSITFTXLSVQVWYIM-----VLS:PNIIITNGCPEDNIHD 191
Db 115 RFOAKYKPKTKYQATTRKRGIALSLVTWAIYAAASFYELMSTNNV--SNKGSQNIIR 172
Oy 192 CSKLSPGLGKMHKTAVTYVNSCP--FVAVLVYLICCYIAISRYIHKSROPIQSRR-- 246
Db 173 CPENYE---KSKPVLIIHICIVLGEFLVETLILPCNIVT---IHTLLRQPKQORNAE 225
Oy 247 -KRKKNQSRVVVNAVFTEFLRPHLCRIFFTPSHDLRLDESAOKLIYKKEITLPLSAC 305
Db 226 VRRRLIMWCYLAFAVIGFVPHHWOLPWTIAELG-MPSSNHQAINDAHQVTLCLIST 284
Oy 306 NVCLDPIIYFPMCRSFSRLPKFSNIRTRSESISIRLSQVARSSEVRIYYDDTV 358
Db 285 NCVLDPIVICYFLTKKRFKLSEGLNIMRSSQKRSRTYTDGTGEMALPINHTPV 337

```

Search completed: June 1, 2004, 15:17:44
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: June 1, 2004, 15:11:49 ; Search time 58 Seconds
(without alignments) 1744.000 Million cell updates/sec

Title: US-09-464-685-1
Perfect score: 1874
Sequence: 1 MGFLTLAKLPNNELHGES.....RSLQSVRSVRIVYDITDV 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*

1: Geneseqp1980a:*
2: Geneseqp1990a:*
3: Geneseqp2000a:*
4: Geneseqp2001a:*
5: Geneseqp2002a:*
6: Geneseqp2003a:*
7: Geneseqp2003bs:*
8: Geneseqp2004a:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1874	100.0	358	AAV45039	AAV45039 Human G p
2	1874	100.0	358	AAV44365	AAV44365 Human G-p
3	1874	100.0	358	AAAB83014	AAAB83014 Human G p
4	1874	100.0	358	AAAB96884	AAAB96884 Human nov
5	1874	100.0	358	AAE03199	AAE03199 Human G-p
6	1874	100.0	358	AAAB67484	AAAB67484 Amino aci
7	1874	100.0	358	ABR48208	ABR48208 Human bla
8	1874	100.0	358	ABUS6683	ABUS6683 Lung cancc
9	1874	100.0	358	ABR01795	ABR01795 Human can
10	1874	100.0	358	ABP81966	ABP81966 Human G p
11	1874	100.0	358	ABU09897	ABU09897 Human G-p
12	1874	100.0	358	AAE34531	AAE34531 Human Mow
13	1874	100.0	358	AAE34534	AAE34534 Human Mow
14	1874	100.0	358	AAE34533	AAE34533 Human Mow
15	1871	99.8	358	AAAB85890	AAAB85890 Human C-P
16	1871	99.8	358	AAAB94659	AAAB94659 Human pro
17	1867	99.6	358	AAE02499	AAE02499 Human CON
18	1863.5	99.4	358	ABUS6480	ABUS6480 Lung cancc
19	1855	99.0	384	AAAB84205	AAAB84205 Amino aci
20	1846	98.5	358	AAV28280	AAV28280 Human G-p
21	1846	98.5	358	ABG77171	ABG77171 Prostate
22	1846	98.5	358	ABUS7629	ABUS7629 Different
23	1846	98.5	358	ADC33516	ADC33516 Human G p
24	1840	98.2	358	AAAB6092	AAAB6092 Human G p
25	1731	92.4	358	AAE34532	AAE34532 Mouse Mow

26	1685	89.9	346	AAE34535	AAE34535 Human Mow
27	889	47.4	196	ABB90283	ABB90283 Human pol
28	768.5	41.0	338	AAV58237	AAV58237 Human KIA
29	768.5	41.0	338	AAE04388	AAE04388 Human UDP
30	768.5	41.0	338	AAU84287	AAU84287 Human end
31	768.5	41.0	338	ABB80778	ABB80778 Human ace
32	768.5	41.0	338	ABP81864	ABP81864 Human UDP
33	768.5	41.0	338	ADC35172	ADC35172 Human GPR
34	768.5	41.0	338	ADC33525	ADC33525 Human KIA
35	768.5	41.0	338	ADG62976	ADG62976 Human KIA
36	762.5	40.7	325	ABU63239	ABU63239 Human G-p
37	742.5	39.6	338	AAV94270	AAV94270 Mouse 7-c
38	742.5	39.6	338	ABB80779	ABB80779 Mouse ace
39	735.5	39.2	338	AAV97541	AAV97541 Rat KIAA0
40	703.5	37.5	333	ADC55385	ADC55385 Human pur
41	700.5	37.4	343	AAE04384	AAE04384 Rat P2-pu
42	700.5	37.4	343	ABP70856	ABP70856 Murine G
43	696	37.1	347	AAAB8354	AAAB8354 Murine G
44	696	37.1	347	ABP70855	ABP70855 Murine P2
45	694.5	37.1	342	AAW81576	AAW81576 EBV-induc

ALIGNMENTS

RESULT 1
AAV45039
ID AAV45039 standard; protein, 358 AA.
XX
AC AAV45039;
XX
DT 31-MAY-2000 (first entry)
XX
DE Human G protein-coupled receptor, HG03.
XX
KW HG03; G protein-coupled receptor; GPCR; screen; agonist; antagonist;
KW pharmaceutical; gene therapy; human.
XX
OS Homo sapiens.
XX
PN WO200008133-A1.
XX
PD 17-FEB-2000.
XX
PF 02-AUG-1999; 99WO-US017388.
XX
PR 06-AUG-1998; 98US-0095571P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Liu Q, McDonald TP, Wang R;
XX
DR WPI; 2000-205701/18.
XX
N-PSDB; AA250776.
XX
PT Novel G-protein coupled receptor cDNA molecule encoding HG03 polypeptide
PT useful for identifying its agonists and antagonists which are useful in
PT pharmaceuticals.
XX
PS Claim 1; Fig 2; 36pp; English.
XX
CC The present sequence is human HG03 protein, which is a G protein-coupled
CC receptor (GPCR). It shows homology to human platelet activating factor
CC receptor (GPR). It is expressed at high levels in prostate, placenta and
CC trachea and at low levels in thymus and testis. HG03 expression vectors
CC can be used to transform host cells, which may be used in screening for
CC agonists or antagonists that are potential pharmaceuticals. It can be
CC used in gene therapy for treatment of diseases associated with low HG03
CC activity.
XX
SQ Sequence 358 AA;
XX
Query Match 100.0%; Score 1874; DB 3; Length 358;

Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGPNLTAKLPNNELHGOESHNSGNSRSDPGKNTLHNEPDTIVLPVYLIIIFVASILLN 60
XX |||||||
CC 1 MGPNLTAKLPNNELHGOESHNSGNSRSDPGKNTLHNEPDTIVLPVYLIIIFVASILLN 60
CC |||||||
CC The present sequence is G-protein coupled receptor designated 2871. This
CC is expressed in prostate, uterus and placenta and participates in
CC signalling pathway. The receptor polypeptide is useful in drug screening
CC assays, and to identify modulating agents. Epitope bearing peptides are
CC used to raise specific antibodies. The polypeptide and modulating agents
CC can also be used for the modulation, diagnosis or treatment of immune or
CC respiratory disorders, e.g. Crohn's disease, multiple sclerosis, asthma,
CC allergies, viral, bacterial or parasitic infections, cystic fibrosis,
CC pneumonia, Legionnaires disease or sinusitis
CC
XX
SQ Sequence 358 AA;

QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRYIHKSROF 240
DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRYIHKSROF 240
QY 241 ISQSRKRRKHNSIRVVAVVFTCTCLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
DB 241 ISQSRKRRKHNSIRVVAVVFTCTCLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358

```

RESULT 2

AA44365
ID AA44365 standard; protein; 358 AA.

XX AA44365;
DT 14-MAR-2000 (first entry)

DE Human G-protein coupled 2871 receptor protein.

KW GPCR; G-protein coupled receptor; signalling pathway;
KW drug screening assay; immune disorder; respiratory disorder;
KW Crohn's disease; multiple sclerosis; asthma; allergy; viral infection;
KW bacterial infection; parasitic infection; cystic fibrosis; pneumonia;
KW Legionnaires disease; sinusitis.

XX Homo sapiens.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..42 /label= Extracellular_domain

FT Domain 43..318 /label= Transmembrane_domain

FT Region 138..140 /note= "GPCR signal transduction signature"

FT Domain 319..359 /label= Intracellular_domain

XX WO963087-A1.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012203.

XX 02-JUN-1999; 98US-00088857.

XX (MILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA, Hodg MR;

XX WPI; 2000-105698/09.

XX DR N-PSDB; AA229524.

XX Isolated human nucleic acid encoding a novel G-protein coupled receptor
XX useful for the modulation, diagnosis or treatment of immune or

PT respiratory disorders.
XX
XX Claim 1; Fig 1; 79pp; English.

CC The present sequence is G-protein coupled receptor designated 2871. This
CC is expressed in prostate, uterus and placenta and participates in
CC signalling pathway. The receptor polypeptide is useful in drug screening
CC assays, and to identify modulating agents. Epitope bearing peptides are
CC used to raise specific antibodies. The polypeptide and modulating agents
CC can also be used for the modulation, diagnosis or treatment of immune or
CC respiratory disorders, e.g. Crohn's disease, multiple sclerosis, asthma,
CC allergies, viral, bacterial or parasitic infections, cystic fibrosis,
CC pneumonia, Legionnaires disease or sinusitis
CC
XX
SQ Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 3; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGPNLTAKLPNNELHGOESHNSGNSRSDPGKNTLHNEPDTIVLPVYLIIIFVASILLN 60
DB 1 MGPNLTAKLPNNELHGOESHNSGNSRSDPGKNTLHNEPDTIVLPVYLIIIFVASILLN 60
QY 61 GLAVWIFPHIRNKTSFIYLNKNIIVADLIMTLTPPFRIVHDAGFGPMWFKFLCYTSVL 120
DB 61 GLAVWIFPHIRNKTSFIYLNKNIIVADLIMTLTPPFRIVHDAGFGPMWFKFLCYTSVL 120
QY 121 FYANNMTSIVFLGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
DB 121 FYANNMTSIVFLGLISIDRYLKVKVPFGDSRMYSITFPKVLSCVWVIMAVLSLPIIILT 180
QY 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRYIHKSROF 240
DB 181 NGOPTEDNIHDCSKLSPGVKMTAVTVNSCLFVAVLVILIGCYIAISRYIHKSROF 240
QY 241 ISQSRKRRKHNSIRVVAVVFTCTCLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
DB 241 ISQSRKRRKHNSIRVVAVVFTCTCLPYHLCRIPFTFSHLDRLLDESAOKILYYCKEITL 300
QY 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358
DB 301 FLSACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRLSQVRSEVRITYYDTDV 358

```

RESULT 3

AA83014
ID AA83014 standard; protein; 358 AA.

XX AA83014;

XX 22-JUN-2001 (first entry)

DE Human G protein coupled receptor HOKR2.

KW Human; HOKR2; G protein coupled receptor; antiinflammatory; antiallergic;
KW immune disease; inflammatory disease; bronchitis; allergy.

XX Homo sapiens.

XX JP2001029084-A.

XX 06-FEB-2001.

XX 23-JUL-1999; 99JP-00209919.

XX 23-JUL-1999; 99JP-00209919.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX WPI; 2001-303765/32.

XX DR N-PSDB; AA82359.

PT Novel G protein coupled receptor, and a gene of the G protein coupled
 PT receptor, useful for screening for agents to prevent and treat
 PT inflammatory diseases such as bronchitis.

PS Claim 1; Page 10-11; 13pp; Japanese.

CC The present sequence is a novel human G protein coupled receptor
 CC designated HOKK2. The total length HOKK2 cDNA was obtained by reverse
 CC transcription-polymerase chain reaction (RT-PCR) using human spleen
 CC derived mRNA as the template. The G protein coupled receptor may be used
 CC to screen for agents that are useful in the prevention and treatment of
 CC immune diseases and inflammatory diseases such as bronchitis and allergy

XX Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPNITLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVYLIFVASIILN 60
 DB 1 MGPNITLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVYLIFVASIILN 60
 QY 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMWPKFLICRYTSL 120
 DB 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMWPKFLICRYTSL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSROF 240
 DB 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSROF 240
 QY 241 ISQSRKKRKHNSIRVVAVVFTCPFLPYHLCRIPFTFSHLDBLDESQOKILYCKEITL 300
 DB 241 ISQSRKKRKHNSIRVVAVVFTCPFLPYHLCRIPFTFSHLDBLDESQOKILYCKEITL 300
 QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358

RESULT 4

AAB96884
 ID AAB96884 standard; protein; 358 AA.

XX AAB96884;

DT 13-JUL-2001 (first entry)

XX Human novel G-protein coupled receptor.

DE Human novel G-protein coupled receptor; disease screening; immune disease;

XX Human; G-protein coupled receptor; bronchitis; allergy.

OS Homo sapiens.

PN JP2001054388-A.

XX 27-FEB-2001.

PF 17-AUG-1999; 99JP-00230776.

PR 17-AUG-1999; 99JP-00230776.

PA (YAMA) YAMANOUCHI PHARM CO LTD.

DR WPI; 2001-321038/34.

XX N-PSDB; AAB96885.

PT A new G protein coupled receptor and G protein coupled receptor gene.

XX Claim 1; Page 10-11; 14pp; Japanese.

CC The present invention provides the protein and coding sequences of a
 CC novel human G-protein coupled receptor. This is useful as a screening
 CC tool for preventive and treatment agents of immune inflammatory diseases
 CC such as bronchitis and allergies. The present sequence is the protein of
 CC the invention

XX Sequence 358 AA;

Query Match 100.0%; Score 1874; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGPNITLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVYLIFVASIILN 60
 DB 1 MGPNITLAKLPNNELHGOESHNSGNSRSDGPKNTTLHNEPDTIVLPVYLIFVASIILN 60
 QY 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMWPKFLICRYTSL 120
 DB 61 GLAVWIFPHIRNKTSFIYLNKIVVADLIMLTLPFRIVHDAGFGPMWPKFLICRYTSL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVKVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSROF 240
 DB 181 NGQPTEDNIHDSCKLSPGVKMTAVTVVNSCLFVAVALVILIGCYIAISRYIHKSROF 240
 QY 241 ISQSRKKRKHNSIRVVAVVFTCPFLPYHLCRIPFTFSHLDBLDESQOKILYCKEITL 300
 DB 241 ISQSRKKRKHNSIRVVAVVFTCPFLPYHLCRIPFTFSHLDBLDESQOKILYCKEITL 300
 QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTSSESIRLSQSVRSEVRYYDYTDV 358

RESULT 5

AAB03199
 ID AAB03199 standard; protein; 358 AA.

XX AAB03199;

DT 03-AUG-2001 (first entry)

XX Human G-protein coupled receptor 2871.

DE Human; G-protein coupled receptor; 2871 receptor; therapy;
 XX immune disorder; respiratory disorder; haematopoietic disorder;
 XX bone marrow disorder; brain disorder; heart disorder; kidney disorder;
 XX blood vessel disorder; prostate disorder; skeletal muscle disorder;
 XX ovary disorder; epididymis disorder; spleen disorder; liver disorder;
 XX T-cells related disorder; thymus related disorder; breast disorder;
 XX B cells related disorder; thyroid disorder; pancreas disorder;
 XX precursor T cell neoplasm related disorder; antineoplastic;
 XX antidiabetic; antifungal; antiparasitic; antiviral; ophthalmological;
 XX antibacterial; antihelminthic; antipneumatic; antifungal; cytostatic;
 XX antihemorrhagic; neuroprotective; neoplastic; antineoplastic; vasotropic;
 XX hepatotropic; immunosuppressive; anxiolytic; hypotensive; cardiac;
 XX antidiabetic; nephrotropic; virostatic; thrombolytic; haemostatic;
 XX human immunodeficiency virus; anti-HIV; dermatological; thyromimetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..42

FT Domain /label= Extracellular_domain

FT Domain 43..318

FT Region /label= Transmembrane_domain

FT Region 138..140

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FT      Domain /label= GPCR_signal_transduction_signature
FT      319..358 /label= Intracellular_domain
XX      MO200144474-A1.
XX      21-JUN-2001.
PD      18-DEC-2000; 2000MO-US035004.
PF      16-DEC-1999; 99US-00464685.
PR      (MILL-) MILLENNIUM PHARM INC.
XX      Glucksmann MA, Hodge MR, Hunter JJ, Rudolph-Owen L, Welch NS;
XX      MPI, 2001-390250/41.
XX      N-PSDB; AAD06915.
XX      Identifying inhibitors or modulators of novel protein, 2871 receptor, a G
XX      protein coupled receptor, useful for treating Crohn's disease, insulin
XX      dependent diabetes mellitus, multiple sclerosis, bronchial asthma.
XX      Claim 1; Fig 1A-ID; 107pp; English.
XX      The present sequence is a human G-protein coupled receptor, 2871
XX      receptor. The 2871 receptor is used for screening a compound that acts as
XX      agonist and antagonist to 2871 receptor. The compounds can be used for
XX      treating disorders such as immune disorders (e.g., asthma and glomerular
XX      nephritis), respiratory disorders (e.g., bronchitis and cystic fibrosis),
XX      haematopoietic disorders involving cells of leukocyte, erythrocyte and
XX      platelet lineages, bone marrow disorders (e.g., leukaemias and lymphoma),
XX      brain disorders (e.g., intracranial haemorrhage, acute meningitis,
XX      multiple sclerosis and Alzheimer's disease), heart disorders (e.g.,
XX      rheumatic heart disease, angina pectoris and myocardial infarction),
XX      blood vessel disorders (e.g., atherosclerosis and hypertension), kidney
XX      disorders (e.g., autosomal recessive polycystic kidney disease, acquired
XX      cystic disease and Heymann nephritis), prostate disorders (e.g., nodular
XX      hyperplasia and carcinoma), skeletal muscle disorders (e.g.,
XX      rhabdomyosarcoma), ovary disorders (e.g., ovarian tumour,
XX      cystadenofibroma), testis and epididymis disorders (e.g., gonorrhoea,
XX      mumps and syphilis), spleen disorders (e.g., congestive splenomegaly and
XX      congenital anomalies), liver disorders (e.g., autoimmune hepatitis and
XX      cirrhosis), T-cells related-disorders (e.g., acquired immunodeficiency
XX      syndrome (AIDS) and inflammatory myopathies), thymus related-disorders
XX      (e.g., thymic cysts and germ cell tumours), B cells related-disorders
XX      (e.g., follicular lymphoma and multiple myeloma), breast related-
XX      disorders (e.g., fat necrosis and fibrocystic changes), thyroid disorders
XX      (e.g., cretinism and myxedema), pancreas disorders (e.g., pancreatitis
XX      and diabetes mellitus) and precursor T cell neoplasm related-disorders
XX      (e.g., T-cell chronic lymphocytic leukaemia)
XX      Sequence 358 AA;
SQ
Query Match 100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      241 ISOSRRKRKHNSIRVWVAVPTCELPYHICRIPTFESHLDRLDESOKILYYCKEITL 300
DB      241 ISOSRRKRKHNSIRVWVAVPTCELPYHICRIPTFESHLDRLDESOKILYYCKEITL 300
QY      301 FLASACNVCDPIITVEFMCGRSFRRLLFKKSNIRTSSESIRLSQSVARSEVRITYDYTDV 358
DB      301 FLASACNVCDPIITVEFMCGRSFRRLLFKKSNIRTSSESIRLSQSVARSEVRITYDYTDV 358
RESULT 6
AA067484
ID      AA067484 strand; protein, 358 AA.
XX
AC      AA067484;
XX
DT      15-MAY-2001 (first entry)
XX
DE      Amino acid sequence of a human oocyte polypeptide.
XX
KW      Human; oocyte; G-protein coupled receptor; infection; pain; cancer;
KW      diabetes; obesity; anorexia; bulimia; asthma; Parkinson's disease;
KW      acute heart failure; hypotension; hypertension; urinary retention;
KW      osteoporosis; angina pectoris; myocardial infarction; stroke; ulcer;
KW      allergy; benign prostatic hypertrophy; migraine; vomiting;
KW      psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW      manic depression; depression; delirium; dementia; mental retardation;
KW      dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome.
XX
OS      Homo sapiens.
XX
PN      WO200109166-A1.
XX
PD      08-FEB-2001.
XX
PF      21-JUL-2000; 2000MO-US020005.
XX
PR      29-JUL-1999; 99US-00363203.
XX
PA      (SMK) SMITHKLINE BEECHAM CORP.
XX
PI      Bergsma DJ, Elshourbagy NA, Guerrero SF, Gattu N, Mooney JL,
PI      Vawter L;
XX
DR      MPI; 2001-182933/18.
XX
N-PSDB; AAF55101.
XX
PT      Novel oocyte polypeptides and polynucleotides encoding a G-protein
PT      coupled receptor for diagnosis and treatment of bacterial infections,
PT      cancer, neurological disorders, obesity and for identifying agonists and
PT      antagonists.
XX
PS      Claim 1; Page 27-28; 31pp; English.
XX
XX      The present sequence represents a human oocyte polypeptide. Oocyte is a
XX      member of the G-protein coupled receptor family. Oocyte polypeptides,
XX      polynucleotides and antibodies are useful for diagnosis and treatment of
XX      certain diseases, including bacterial, fungal, protozoan and viral
XX      infections, particularly infections caused by HIV-1 and HIV-2, pain,
XX      cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
XX      disease, acute heart failure, hypotension, hypertension, urinary
XX      retention, osteoporosis, angina pectoris, myocardial infarction, stroke,
XX      ulcers, allergies, benign prostatic hypertrophy, migraine, vomiting,
XX      psychotic and neurological disorders, including anxiety, schizophrenia,
XX      manic depression, depression, delirium, dementia, and severe mental
XX      retardation, dyskinesia, such as Huntington's disease or Gilles de la
XX      Tourette's syndrome
XX
SQ      Sequence 358 AA;
Query Match 100.0%; Score 1874; DB 4; Length 358;
Best Local Similarity 100.0%; Pred. No. 6.6e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 MGFNLTAKL.PNNELHGOESHNSGRSDPGKNTTLHNEPPTIVL.PVLYLIIFVASILLN 60
 DB 1 MGFNLTAKL.PNNELHGOESHNSGRSDPGKNTTLHNEPPTIVL.PVLYLIIFVASILLN 60
 QY 61 GLAWIIFPHINKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMYFKFLCRYSVL 120
 DB 61 GLAWIIFPHINKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMYFKFLCRYSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGLGYKMTAVTYVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGLGYKMTAVTYVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 QY 241 ISOSRRKKKNQSIIRVVAVVFTCP.PYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 DB 241 ISOSRRKKKNQSIIRVVAVVFTCP.PYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVARSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVARSEVRYYDYTDV 358

RESULT 7
 ABR48208
 ID ABR48208 standard; protein, 358 AA.
 XX ABR48208;
 DT 12-JUN-2003 (first entry)
 XX Human bladder cancer associated protein sequence SEQ ID NO:135.
 XX Human; bladder cancer; cytostatic; gene therapy; vaccine.
 XX Homo sapiens.
 PN MO2003003906-A2.
 PD 16-JAN-2003.
 XX 03-JUL-2002; 2002WO-US021338.
 PR 03-AUG-2001; 2001US-0302814P.
 PR 08-NOV-2001; 2001US-0343705P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 12-APR-2002; 2002US-0372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI Mack DH, Aziz N;
 DR WPI; 2003-201532/19.
 DR N-PSDB; ACC51022.
 PT Detecting a bladder cancer-associated transcript in a cell from a
 PT patient, comprises contacting a biological sample from the patient with a
 PT bladder cancer-associated polynucleotide or antibody.
 XX Claim 10; Page 277; 307pp; English.
 PS The present invention describes a method for detecting a bladder cancer-
 XX associated transcript in a cell from a patient. The method comprises
 CC contacting a biological sample from the patient with a polynucleotide
 CC that selectively hybridizes to a sequence that is 80 % identical to a
 CC table of sequences (see ACC50951 to ACC51059). ACC50951 to ACC51059
 CC encode the human bladder cancer-associated proteins given in ABR48146 to
 CC ABR48242). Bladder cancer-associated sequences from the present invention
 CC have cytostatic activities, and can be used in antisense gene therapy and

CC in vaccine production. The method can be used for detecting a bladder
 CC cancer-associated transcript in a cell from a patient. The method is
 CC useful in diagnosing or treating bladder cancer and in screening for
 CC compounds that modulate bladder cancer, such as hormones or antibodies.
 CC The nucleic acid molecules from the present invention may be used in
 CC various screening and diagnostic methods, and for gene therapy, vaccine
 CC and/or antisense/inhibition applications

SO Sequence 358 AA;
 Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGFNLTAKL.PNNELHGOESHNSGRSDPGKNTTLHNEPPTIVL.PVLYLIIFVASILLN 60
 DB 1 MGFNLTAKL.PNNELHGOESHNSGRSDPGKNTTLHNEPPTIVL.PVLYLIIFVASILLN 60
 QY 61 GLAWIIFPHINKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMYFKFLCRYSVL 120
 DB 61 GLAWIIFPHINKTSFIYLNKNIIVADLIMLTLPFRIVHDAGFGPMYFKFLCRYSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVVKPFQDSRMYSITFTKVLSCVWVIMAVLSLPIIILT 180
 QY 181 NGOPTEDNIHDCSKLSPGLGYKMTAVTYVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPGLGYKMTAVTYVNSCLFVAVLVLLIGCYIAISRIRHSSROF 240
 QY 241 ISOSRRKKKNQSIIRVVAVVFTCP.PYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 DB 241 ISOSRRKKKNQSIIRVVAVVFTCP.PYHLGRIPFTFPHLDRLDESAOKILYYCKEITL 300
 QY 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVARSEVRYYDYTDV 358
 DB 301 FLSACNVCLDPIIYFFMCRSFSRRLFKKSNIRTRSESIRLSQSVARSEVRYYDYTDV 358

RESULT 8
 ABUS6683
 ID ABUS6683 standard; protein, 358 AA.
 XX ABUS6683;
 DT 02-APR-2003 (first entry)
 XX Lung cancer-associated polypeptide #276.
 XX Lung cancer-associated polypeptide #276.
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antineoplastic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS
 XX
 XX
 XX WO200286443-A2.
 PD 31-OCT-2002.
 PD 18-APR-2002; 2002WO-US012476.
 PR 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0230492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.
 PR 12-APR-2002; 2002US-0372246P.
 PA (EOSB-) EOS BIOTECHNOLOGY INC.
 PI Aziz N, Murray R;

XX MPI: 2003-093161/08.
 DR N-PSDB; ABX76412.
 PT Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 XX expression in lung cancer.
 XX
 PS Claim 27; Page 400; 453pp; English.
 CC The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX
 SQ Sequence 358 AA;
 Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTLLHNEFTIVLPVLYLIIFVASILLN 60
 DB 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTLLHNEFTIVLPVLYLIIFVASILLN 60
 QY 61 GLAWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPWFYFKILCRYTSVL 120
 DB 61 GLAWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPWFYFKILCRYTSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGOPTEDNIDHCSKLSPLGVKMTAVTYVNSCLFVAVVILIGCYIAISRYIHKSROF 240
 DB 181 NGOPTEDNIDHCSKLSPLGVKMTAVTYVNSCLFVAVVILIGCYIAISRYIHKSROF 240
 QY 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTHLDRLLDESAOKILVYCKEITL 300
 DB 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTHLDRLLDESAOKILVYCKEITL 300
 QY 301 FLASACNVCLDPIITYFPCRSFSRRLFKKSNIRTRSEISIRLSQVRSREVIYYDYTDV 358
 DB 301 FLASACNVCLDPIITYFPCRSFSRRLFKKSNIRTRSEISIRLSQVRSREVIYYDYTDV 358
 RESULT 9
 ID ABR01795 standard; protein; 358 AA.
 XX ABR01795;
 XX 19-MAY-2003 (first entry)
 XX Human cancer-related protein, 154P2A8.
 XX Human; cytosolic; vaccine; cancer; immune response.
 KW

XX Homo sapiens.
 OS WO200283921-A2.
 XX
 XX 24-OCT-2002.
 XX
 XX 10-APR-2002; 2002WO-US011654.
 XX
 XX 10-APR-2001; 2001US-0282739P.
 PR 10-APR-2001; 2001US-0283112P.
 PR 25-APR-2001; 2001US-0286630P.
 XX
 PA (AGEN-) AGENSYS INC.
 PI Jakobovits A, Challita-Eid PM, Farris M, Ge W, Hubert RS;
 PI Morrison K, Morrison RK, Raitano AB;
 DR MPI: 2003-075555/07.
 DR N-PSDB; ABZ78126.
 XX
 XX New composition comprising a substance that modulates the structure of
 PT proteins and polynucleotides, useful for therapeutic, prognostic and
 PT diagnostic reagents for eliciting cellular or humoral immune response in
 PT cancer patients.
 XX
 PS Claim 12; Fig 2F, 1021pp; English.
 CC The present invention relates to novel human cancer-related genes and
 CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
 CC proteins are useful for eliciting a humoral or cellular immune response.
 CC The genes are useful as probes and primers for the amplification and/or
 CC detection of genes, mRNAs or their fragments, as reagents for the
 CC diagnosis and/or prognosis of cancer, as coding sequences capable of
 CC directing the expression of the protein, as tools for modulating or
 CC inhibiting the expression of genes and/or translation of transcripts, and
 CC as therapeutic agents. The proteins and peptides are useful as
 CC therapeutic, prognostic and diagnostic reagents for cancer
 CC
 XX
 SQ Sequence 358 AA;
 Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTLLHNEFTIVLPVLYLIIFVASILLN 60
 DB 1 MGFNLTLLAKLPNNELHGOESHNSGNRSDGPKNTLLHNEFTIVLPVLYLIIFVASILLN 60
 QY 61 GLAWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPWFYFKILCRYTSVL 120
 DB 61 GLAWIFPHIRNKTSFIPLYKNIVADLIMTLTPFPRIYHDAGFGPWFYFKILCRYTSVL 120
 QY 121 FYANNYTSIVFLGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 DB 121 FYANNYTSIVFLGLISIDRYLKVKRPGDSRMYSITFTKVLSCVWVIMAVLSLNNIILT 180
 QY 181 NGOPTEDNIDHCSKLSPLGVKMTAVTYVNSCLFVAVVILIGCYIAISRYIHKSROF 240
 DB 181 NGOPTEDNIDHCSKLSPLGVKMTAVTYVNSCLFVAVVILIGCYIAISRYIHKSROF 240
 QY 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTHLDRLLDESAOKILVYCKEITL 300
 DB 241 ISOSRRKRKKNOSIRVVAVVFTFCFLPYHLCRIPTFTHLDRLLDESAOKILVYCKEITL 300
 QY 301 FLASACNVCLDPIITYFPCRSFSRRLFKKSNIRTRSEISIRLSQVRSREVIYYDYTDV 358
 DB 301 FLASACNVCLDPIITYFPCRSFSRRLFKKSNIRTRSEISIRLSQVRSREVIYYDYTDV 358
 RESULT 10
 ID ABR01966 standard; protein; 358 AA.
 ABP81966

Human G protein-coupled receptor GPR87/95 protein SEQ ID NO:418.

KM G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KM G protein-coupled receptor modulator; antibody; immune-related disease;
KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
KM immunological-related cell proliferative disease; autoimmune disease;
KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy
KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KM hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KM ulcer.

OS Homo sapiens.

PN W0200261087-A2.

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P.

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

PI Burmer GC, Roush CL, Brown JP;

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42814.

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

PS Disclosure; Fig 1; 523pp; English.

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

SQ Sequence 358 AA;

Query Match	100.0%;	Score 1874;	DB 6;	Length 358,
Best Local Similarity	100.0%;	Pred. No. 6.6e-204;		

Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPNLTIAKL.PNNELHAGSHSGNRSDPGKNTT.LHNFEDTIVL.VL.VL.II.IVASITL.N	60
Db	1	MGPNLTIAKL.PNNELHAGSHSGNRSDPGKNTT.LHNFEDTIVL.VL.VL.II.IVASITL.N	60
QY	61	GLAVMIFPHIRNKTSPIFYLKNI.VVADL.IMLTLP.PRI.VHDAGFGWYEFKIL.CRTYSVL	120
Db	61	GLAVMIFPHIRNKTSPIFYLKNI.VVADL.IMLTLP.PRI.VHDAGFGWYEFKIL.CRTYSVL	120
QY	121	FYANNYSIVF.GLISIDRYLKV.KVPCFGDSRMYSIFFT.KVLSVCWVIMAVLSL.PNII.LT	180
Db	121	FYANNYSIVF.GLISIDRYLKV.KVPCFGDSRMYSIFFT.KVLSVCWVIMAVLSL.PNII.LT	180
QY	181	NGQPLEDNIHDCSKLSP.LGVKMTAA.VTVYNSCL.PYAV.LVILIGCTIY.IISRYTHKKSROF	240
Db	181	NGQPLEDNIHDCSKLSP.LGVKMTAA.VTVYNSCL.PYAV.LVILIGCTIY.IISRYTHKKSROF	240
QY	241	ISQSRKKKHQNS.IIVVVA.VFETCEL.PYHLCRI.PFTFSH.DRLDLDSQAOKILVYCKEITL	300
Db	241	ISQSRKKKHQNS.IIVVVA.VFETCEL.PYHLCRI.PFTFSH.DRLDLDSQAOKILVYCKEITL	300
QY	301	FLSACNVCLDPIIYF.MGRSFSRRL.PKKSNIITR.SSINSLSQVRSRSEVRIYDYDYDV	358
Db	301	FLSACNVCLDPIIYF.MGRSFSRRL.PKKSNIITR.SSINSLSQVRSRSEVRIYDYDYDV	358

RESULT 11

ID ABU09897 standard; protein; 358 AA

AC ABU09897;

DT 11-AUG-2003 (first entry)

DE Human G-protein coupled receptor 2871.

Human, receptor; G-protein coupled receptor; gene therapy; pneumonia; immune disorder; Crohn's disease; Grave's disease; respiratory disorder; diphtheria; haemotopoietic disorder; leukaemia; systemic sclerosis; prostatic disorder; benign prostatic hypertrophy; tumour; breast disease; acute mastitis; Paget's disease; muscular disorder; rhabdomyosarcoma; neurological disorder; cerebral oedema; Parkinson's disease; atrophy; blood vessel disorder; atherosclerosis; testicular disease; epiphallia; epididymal disease; thyroid disease; hyperthyroidism; cretinism; AIDS; kidney disorder; cystic renal dysplasia; glomerulonephritis; cardiovascular disease; heart failure; pericarditis; pancreatic disease; pancreatitis; diabetes mellitus; thymus disease; thymic hypoplasia; Hodgkin disease; spleen disease; splenomegaly; gaucher disease; liver disease; hepatic failure; alcoholic liver disease; T-cell disorder; systemic lupus erythematosus; B-cell disorder; Burkitt lymphoma; multiple myeloma; platelet disorder; thrombocytopenia; haemolytic-uraemic syndrome.

OS Homo sapiens

PN US2003017539-A1.

PD 23-JAN-2003

PF 07-JUN-2002; 2002US-00165844

PR	02-JUN-1998;	98UUS-00088857
PR	02-SEP-1998;	98UUS-00145745
PR	21-JAN-1999;	99UUS-00234923
PR	02-JUN-1999;	99UUS-00324465
PR	28-JUN-1999;	99UUS-00340880
PR	26-AUG-1999;	99UUS-00383745
PR	16-DEC-1999;	99UUS-00466485
PR	18-DEC-2000;	2000UUS-00741783

(MILL-) MILLENNIUM PHARM INC.

XX

PI Glucksmann MA, Hodge MR, Hunter JT, Rudolph-Owen LA;
 PI Siles-Santiago I, Welch NS;
 DR WPI: 2003-401672/38.
 DR N-PSDB; A061170.
 PT New nucleic acid molecule encoding a G-protein coupled receptor
 PT polypeptide, e.g. 2871, 14926, 17723 or 23992, useful for diagnosing
 PT and/or treating cancer or immune, respiratory, hematologic or
 PT cardiovascular disorders.
 XX
 PS Claim 9; Fig 1; 149pp; English.
 XX
 XX The invention relates to an isolated G-protein coupled receptor nucleic
 CC acid molecule encoding the G-protein coupled receptors 2871, 14926, 17723
 CC and 23992. The nucleic acid molecule is useful in monitoring, diagnosing
 CC and treating immune disorders (e.g. Crohn's disease and Grave's disease);
 CC and treating immune disorders (e.g. pneumonia or diptheria); haematopoietic
 CC respiratory disorders (e.g. leukæmia and systemic sclerosis); prostatic disorders
 CC disorders (e.g. leukaemia and systemic sclerosis); breast diseases (e.g.
 CC (e.g. benign prostate hypertrophy and tumours); diseases involving
 CC acute mastitis and Paget's disease); muscular disorders (e.g.
 CC rhabdomyosarcoma); neurological disorders (e.g. cerebral oedema and
 CC Parkinson's disease); disorders involving blood vessels (e.g.
 CC atherosclerosis); diseases involving testis and epididymis (e.g. atrophy
 CC and syphilis); thyroid diseases (e.g. hyperthyroidism and cretinism);
 CC kidney disorders (e.g. cystic renal dysplasia and glomerulonephritis);
 CC cardiovascular diseases (e.g. heart failure and pericarditis); pancreatic
 CC diseases (e.g. pancreaticitis and diabetes mellitus); diseases involving
 CC the thymus (e.g. thymic hypoplasia and Hodgkin disease); diseases
 CC involving the spleen (e.g. splenomegaly and Gaucher disease); T
 CC -cell disorders (e.g. systemic lupus erythematosus and AIDS); B-cell
 CC disorder (e.g. Burkitt lymphoma and multiple myeloma); platelet disorders
 CC (e.g. thrombocytopenia and haemolytic-uraemic syndrome); The nucleic
 CC acids may also be used in chromosome mapping, tissue typing,
 CC pharmacogenomics and forensic biology, and as surrogate markers. The
 CC present sequence represents the amino acid sequence of the human G-
 CC protein coupled receptor 2871
 CC
 XX
 XX Sequence 358 AA;
 SQ
 Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204; Indels 0; Gaps 0;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNLTALAKPNNEHGHGSHNSGNRSDPGKNTTLHNEFDTIVLPVYLIIIFVASTILN 60
 DB 1 MGNLTALAKPNNEHGHGSHNSGNRSDPGKNTTLHNEFDTIVLPVYLIIIFVASTILN 60
 QY 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMLTLPFRIVHAGFGPMWFKFLCRYSVL 120
 DB 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMLTLPFRIVHAGFGPMWFKFLCRYSVL 120
 QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 DB 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 DB 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 QY 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 QY 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 QY 241 ISOSRRKRKHNSIRVVAVVFTFCFLPYHLCRIPFTSHLDRLIDBSAQKILYYCKEITL 300
 DB 241 ISOSRRKRKHNSIRVVAVVFTFCFLPYHLCRIPFTSHLDRLIDBSAQKILYYCKEITL 300
 QY 301 FLSAGNVCLDPIIYFPMCRSFSRRLLFKSNIRTSSESIRLSQVRSSEVAVIYYDYDV 358
 DB 301 FLSAGNVCLDPIIYFPMCRSFSRRLLFKSNIRTSSESIRLSQVRSSEVAVIYYDYDV 358
 RESULT 12
 AAE34531
 ID AAE34531 standard; protein; 358 AA.

XX AAE34531;
 AC 14-MAY-2003 (first entry)
 DT Human Mowgli G-protein coupled receptor #1.
 XX Mowgli G-protein coupled receptor; GPCR; immune response; infection;
 KW neurological disorder; Parkinson's disease; obesity; asthma; cancer;
 KW anorexia; pain; diabetes; vaccine; human.
 XX Homo sapiens.
 OS WO200292624-A2.
 PN 21-NOV-2002.
 PD 16-MAY-2002; 2002WO-GB002304.
 PF 16-MAY-2001; 2001GB-00011959.
 PR 18-MAY-2001; 2001US-0292141P.
 XX (PARA-) PARADIGM THERAPEUTICS LTD.
 PA Carlton M, Aparicio S, Dixon J, Thresher R, Zahn D;
 PI WPI: 2003-129261/12.
 DR N-PSDB; AAD52809.
 XX
 XX New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
 PT useful for inducing immunological response to produce antibody and/or T
 PT cell immune response against e.g. bacterial, fungal, protozoan or viral
 PT infections.
 XX
 PS Claim 1; Page 114-115; 121pp; English.
 XX The invention relates to novel Mowgli G-protein coupled receptor (GPCR)
 CC polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids,
 CC probes, antibodies, expression vectors and ligands are useful as
 CC biosensors, for detection, diagnosis, or treatment of diseases associated
 CC with over-, under- or abnormal expression of Mowgli GPCR in tissues. In
 CC genetic analysis and in chromosome identification. Polypeptides of the
 CC invention may be used for screening compounds which bind the receptor and
 CC which activate (agonists) or inhibit (antagonist) activation of Mowgli.
 CC They may further be used as vaccines to induce immunological response to
 CC produce antibody and/or T cell immune response against e.g. bacterial,
 CC protozoan, fungal or viral infections, pain, cancers, diabetes, obesity,
 CC anorexia, asthma, Parkinson's disease and other neurological disorders.
 CC The present sequence is human Mowgli G-protein coupled receptor
 CC
 XX
 XX Sequence 358 AA;
 SQ
 Query Match 100.0%; Score 1874; DB 6; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.6e-204; Indels 0; Gaps 0;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGNLTALAKPNNEHGHGSHNSGNRSDPGKNTTLHNEFDTIVLPVYLIIIFVASTILN 60
 DB 1 MGNLTALAKPNNEHGHGSHNSGNRSDPGKNTTLHNEFDTIVLPVYLIIIFVASTILN 60
 QY 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMLTLPFRIVHAGFGPMWFKFLCRYSVL 120
 DB 61 GLAWMIFPHIRNKTSIFLYLKNIVVADLIMLTLPFRIVHAGFGPMWFKFLCRYSVL 120
 QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 DB 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 QY 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 DB 121 FYANMTYSIVFLGLISIDRYLKVVPFGDSRMYSITFTKVLSCVWVIMAVLSLNNILT 180
 QY 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 QY 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 DB 181 NGOPTEDNIHDCSKLSPKPLGVKMTAVTYNSCLFPAVAVIILGCIYIAISRYIHSSROF 240
 QY 241 ISOSRRKRKHNSIRVVAVVFTFCFLPYHLCRIPFTSHLDRLIDBSAQKILYYCKEITL 300

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Db      241  ISQSRKRNQSIIRVVAVFTCLPYHLCRIFPTFESHDLRLDESAOKILYYCKEITL 300
Qy      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358
Db      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358

RESULT 13
AAE34534 ID AAE34534 standard; protein; 366 AA.
AC      AAE34534;
XX      14-MAY-2003 (first entry)
XX      Human Mowgli G-protein coupled receptor with FLAG tag.
DE      Mowgli G-protein coupled receptor; GPCR; immune response; infection;
KW      neurological disorder; Parkinson's disease; obesity; asthma; cancer;
KW      anorexia; pain; diabetes; vaccine; human.
XX      Homo sapiens.
OS      Synthetic.
XX      Key
FH      Region 1..358
FT      /note= "Human Mowgli GPCR protein"
FT      Region 359..366
FT      /note= "FLAG tag"
XX      WO200292624-A2.
XX      21-NOV-2002.
XX      16-MAY-2002; 2002WO-GB002304.
XX      16-MAY-2001; 2001GB-00011959.
XX      18-MAY-2001; 2001US-0292141P.
XX      (PARA-) PARADIGM THERAPEUTICS LTD.
XX      PA
XX      Carleton M, Aparicio S, Dixon J, Thresher R, Zahn D;
XX      WPI; 2003-129261/12.
XX      New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
XX      useful for inducing immunological response to produce antibody and/or T
XX      cell immune response against e.g. bacterial, fungal, protozoan or viral
XX      infections.
XX      Claim 1; Page 117-118; 121pp; English.
XX      The invention relates to novel Mowgli G-protein coupled receptor (GPCR)
XX      polypeptides and polynucleotides. Mowgli polypeptides, nucleic acids,
XX      probes, antibodies, expression vectors and ligands are useful as
XX      biosensors, for detection, diagnosis, or treatment of diseases associated
XX      with over- or abnormal expression of Mowgli GPCR in tissues, in
XX      genetic analysis and in chromosome identification. Polypeptides of the
XX      invention may be used for screening compounds which bind the receptor and
XX      which activate (agonists) or inhibit (antagonists) activation of Mowgli.
XX      They may further be used as vaccines to induce immunological response to
XX      produce antibody and/or T cell immune response against e.g. bacterial,
XX      protozoan, fungal or viral infections, pain, cancers, diabetes, obesity,
XX      anorexia, asthma, Parkinson's disease and other neurological disorders.
XX      The present sequence is human Mowgli G-protein coupled receptor with FLAG
XX      tag
XX      Sequence 366 AA;
XX
Query Match 100.0%; Score 1874; DB 6; Length 366;
Best Local Similarity 100.0%; Pred. No. 6,8e-204;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1  MGRNLTLAKLPPNNELHGOESNNSGNSRSDGPKQNTLHNEPPTIVLPVLXLIIPVASILLN 60
Db      1  MGFNLTLAKLPNNELHGOESNNSGNSRSDGPKQNTLHNEPPTIVLPVLXLIIPVASILLN 60
Qy      61  GLAWIFPHIRNKTSFIIFYLNIVADLIMTLTFPPRIVDAGCGPMYFEKILCRYSTVL 120
Db      61  GLAWIFPHIRNKTSFIIFYLNIVADLIMTLTFPPRIVDAGCGPMYFEKILCRYSTVL 120
Qy      121  FYANNYTSIVFLGISIDRYLKVKKPPGDSMYSITTFKVLSCVWMVIMAVLSLPIIILT 180
Db      121  FYANNYTSIVFLGLISIDRYLKVKKPPGDSMYSITTFKVLSCVWMVIMAVLSLPIIILT 180
Qy      181  NGOPTENIHDCSLKSPGLGKVMHTAATYVNSCLFVAALVILIGCYIAISRTHKSRQF 240
Db      181  NGOPTENIHDCSLKSPGLGKVMHTAATYVNSCLFVAALVILIGCYIAISRTHKSRQF 240
Qy      241  ISQSRKRNQSIIRVVAVFTCLPYHLCRIFPTFESHDLRLDESAOKILYYCKEITL 300
Db      241  ISQSRKRNQSIIRVVAVFTCLPYHLCRIFPTFESHDLRLDESAOKILYYCKEITL 300
Qy      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358
Db      301  FLACNVCLDPIIYFPMCRSFSRRLFKKSNIRTSSESIRSLQSVRRSEVRRIYYDTDV 358

RESULT 14
AAE34533 ID AAE34533 standard; protein; 364 AA.
AC      AAE34533;
XX      14-MAY-2003 (first entry)
XX      Human Mowgli G-protein coupled receptor with V5 and His tag.
DE      Mowgli G-protein coupled receptor; GPCR; immune response; infection;
KW      neurological disorder; Parkinson's disease; obesity; asthma; cancer;
KW      anorexia; pain; diabetes; vaccine; human.
XX      Homo sapiens.
OS      Synthetic.
XX      Key
FH      Region 1..364
FT      /note= "Human Mowgli GPCR protein"
FT      Region 365..378
FT      /note= "V5 tag"
FT      Region 379..384
FT      /note= "His tag"
XX      WO200292624-A2.
XX      21-NOV-2002.
XX      16-MAY-2002; 2002WO-GB002304.
XX      16-MAY-2001; 2001GB-00011959.
XX      18-MAY-2001; 2001US-0292141P.
XX      (PARA-) PARADIGM THERAPEUTICS LTD.
XX      PA
XX      Carleton M, Aparicio S, Dixon J, Thresher R, Zahn D;
XX      WPI; 2003-129261/12.
XX      New Mowgli G-protein coupled receptor polypeptides and polynucleotides,
XX      useful for inducing immunological response to produce antibody and/or T
XX      cell immune response against e.g. bacterial, fungal, protozoan or viral
XX      infections.
XX      Claim 1; Page 117; 121pp; English.
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